

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 14:57:06 ; Search time 8.69136 Seconds
(without alignments)
839.896 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLHFWFLLLLLL.....SSVSNPRNWLFLMLIVFCI 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000	100.0	176	1	TR23_MOUSE
2	705	70.5	180	1	TR22_MOUSE
3	226.5	22.7	332	1	TNR6_PIG
4	219.5	21.9	323	1	TNR6_BOVIN
5	215.5	21.6	454	1	TR1A_MOUSE
6	211.5	21.1	351	1	CRMB_COMPX
7	210	21.0	461	1	TR1A_RAT
8	208.5	20.8	349	1	CRMB_CAMPS
9	205.5	20.5	455	1	TR1A_HUMAN
10	205	20.5	327	1	TNR6_MOUSE
11	202.5	20.2	349	1	CRMB_VARY
12	196	19.6	471	1	TR1A_BOVIN
13	194	19.4	324	1	TNR6_RAT
14	193.5	19.4	461	1	TR1A_PIG
15	189.5	18.9	335	1	TNR6_HUMAN
16	186	18.6	417	1	TR16_MOUSE
17	183	18.3	427	1	TR16_HUMAN
18	181	18.1	655	1	TR21_MOUSE
19	175	17.5	655	1	TR21_HUMAN
20	171	17.1	425	1	TR16_RAT
21	168	16.8	283	1	TR14_HUMAN
22	167.5	16.8	300	1	TR6B_HUMAN
23	167.5	16.8	326	1	VT2_MYXVL
24	166.5	16.7	416	1	TR16_CHICK
25	164.5	16.4	386	1	T10D_HUMAN
26	164.5	16.4	417	1	TR12_HUMAN
27	164	16.4	325	1	VT2_SFVKA
28	162.5	16.2	381	1	T10B_MOUSE
29	161.5	16.2	259	1	T10C_HUMAN
30	160.5	16.1	416	1	TR19_MOUSE
31	156	15.6	468	1	T10A_HUMAN
32	155	15.5	401	1	T11B_RAT
33	152	15.2	461	1	TR1B_HUMAN
34	150.5	15.0	415	1	TNR3_MOUSE
35	150	15.0	271	1	TNR4_RAT
36	150	15.0	401	1	T11B_MOUSE
37	150	15.0	435	1	TNR3_HUMAN
38	149	14.9	595	1	TNR8_HUMAN
39	148	14.8	250	1	TNR7_MOUSE
40	145	14.5	260	1	TNR7_HUMAN
41	145	14.5	474	1	TR1B_MOUSE
42	145	14.5	498	1	TNR8_MOUSE
43	144	14.4	277	1	TNR4_HUMAN
44	144	14.4	401	1	T11B_HUMAN
45	140.5	14.1	493	1	TNR8_RAT

RESULT 1

ID	TR23_MOUSE	STANDARD;	PRT;	176 AA.
AC	Q9ER63; Q9VHCO;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).			
GN	TNFRSF23 OR TNFRSF1A11 OR TNFRH1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/Sv; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.;			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting.";			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	Pan G., Mao W., Risser P.;			
RT	"Characterization of SOB, a member of the TNFR family ";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).			
CC	-!- TISSUE SPECIFICITY: Ubiquitous.			
CC	-!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.			
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CC	EMBL; AJ278264; CAC16405.1; -			
DR	EMBL; AJ276505; CAC27352.1; -			
DR	EMBL; AY046550; AAL05072.1; -			
DR	HSSP; P19438; 1EXT.			
DR	MGI; MGI:1930269; Tnfrsf23.			
DR	InterPro; IPR001368; TNFR_C6.			
DR	Pfam; PF00020; TNFR_C6; 3.			
DR	SMART; SM00208; TNFR; 3.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.			
FT	DOMAIN 1 9			
FT	TRANSMEM 10 30			
FT	CYTOSOLIC (POTENTIAL).			
FT	SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).			
FT	DOMAIN 31 176			
FT	EXTRACELLULAR (POTENTIAL).			
FT	REPEAT 37 72			
FT	TNFR-CYS 1.			
FT	REPEAT 74 114			
FT	TNFR-CYS 2.			

ALIGNMENTS

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FT REPEAT 115 155 TNFR-CYS 3
FT DISULFID 38 49 BY SIMILARITY.
FT FT 50 63 BY SIMILARITY.
FT FT 53 72 BY SIMILARITY.
FT FT 75 90 BY SIMILARITY.
FT FT 93 106 BY SIMILARITY.
FT FT 106 114 BY SIMILARITY.
FT FT 116 131 BY SIMILARITY.
FT FT 134 147 BY SIMILARITY.
FT FT 137 155 BY SIMILARITY.
FT FT 148 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 176 AA; 19594 MW; E30D617F49DDB7D CRC64;

Query Match
Best Local Similarity 100.0%; Score 1000; DB 1; Length 176;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYTSHVSSLHWFLLLLLLLLLLFLPVIFAMPESYFNCNCPDGEYQSNVDCCKCPGSGTFVK 60
Db 1 MYTSHVSSLHWFLLLLLLLLLLFLPVIFAMPESYFNCNCPDGEYQSNVDCCKCPGSGTFVK 60

QY 61 APCPKIPHTQGOCEKCHPGTFTGKDNGLHDCCLSTCDKDONNVADCSATSDRKCECOIGL 120
Db 61 APCPKIPHTQGOCEKCHPGTFTGKDNGLHDCCLSTCDKDONNVADCSATSDRKCECOIGL 120

QY 121 YYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSYSSVSNPRNWLFLMLLIVFCI 176
Db 121 YYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSYSSVSNPRNWLFLMLLIVFCI 176

RESULT 2
TR22_MOUSE STANDARD; PRT; 180 AA.
AC Q9R62; Q9CZ44; Q8VHB9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis
GN factor receptor p60 homolog 2) (TNF receptor family member SOBA).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=129/SV; TISSUE=Embryonic stem cells;
RC MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RX Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RL Implications for a novel imprinting centre and extended imprinting.";
RN Hum. Mol. Genet. 9:2691-2706(2000).
[2]
SEQUENCE FROM N.A.
RP Rissler P., Mao W., Baldwin D.T., Pan G.;
RA "Characterization of SOBA, a murine member of the TNFR family.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyok-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; AJ278265; CAC16406.1; -
DR EMBL; AJ276505; CAC27353.1; -
DR EMBL; AY046551; AAL05073.1; -
DR EMBL; AK012838; BAB28502.1; -
DR HSSP; P19438; 1EXT.
DR MGD; MGI:1930270; Tnfrsf22.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 42 180 EXTRACELLULAR (POTENTIAL).
FT REPEAT 47 82 TNFR-CYS 1.
FT REPEAT 84 124 TNFR-CYS 2.
FT REPEAT 125 165 TNFR-CYS 3.
FT DISULFID 48 59 BY SIMILARITY.
FT DISULFID 60 73 BY SIMILARITY.
FT DISULFID 63 82 BY SIMILARITY.
FT DISULFID 85 100 BY SIMILARITY.
FT DISULFID 103 116 BY SIMILARITY.
FT DISULFID 106 124 BY SIMILARITY.
FT DISULFID 126 141 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 147 165 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 12 12 L->V (IN REF. 3).
FT CONFLICT 171 180 RRSASVANFI->NPRNRLFLLL (IN REF. 2).
SQ SEQUENCE 180 AA; 20226 MW; F8F56E165ADD53FA CRC64;

Query Match
Best Local Similarity 70.5%; Score 705; DB 1; Length 180;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 5 SHVSSLHWFL-----LLLLLLNLFLPVIFAMPESYFNCNCPDGEYQSNVDCCKCPG 56
Db 7 SLVSSLRWFLWRRLLRLLLLLLLNLPLQVKFAMLELHSEKCPAGEYKSWDKCKNCAG 66

QY 57 TFVKAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCCLSTCDKDONNVADCSATSDRKCEC 116
Db 67 TFVKAPCEIPHTQGOCEKCHPGTFTGKDNGLHDCCLSTCDKDONNVADCSATSDRKCEC 126

QY 117 QIGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSYSSVSN 160
Db 127 RTGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSYSSVSN 170

RESULT 3
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DR	PROSITE; PS00652;	TNFR_NGFR_1;	2.
DR	PROSITE; PS00500;	TNFR_NGFR_2;	3.
DR	PROSITE; PSS0017;	DEATH_DOMAIN;	1.
KW	Receptor; Apoptosis; Glycoprotein;	Transmembrane; Repeat; Signal.	
FT	SIGNAL	1	16
FT	CHAIN	17	323
FT	DOMAIN	17	170
FT	TRANSSEM	171	188
FT	DOMAIN	189	323
FT	REPEAT	45	80
FT	REPEAT	81	124
FT	REPEAT	125	163
FT	DOMAIN	238	306
FT	DISULFID	45	56
FT	DISULFID	57	70
FT	DISULFID	60	79
FT	DISULFID	82	98
FT	DISULFID	101	116
FT	DISULFID	104	124
FT	DISULFID	126	140
FT	DISULFID	143	154
FT	DISULFID	146	162
FT	CARBOHYD	38	38
FT	CARBOHYD	115	115
SQ	SEQUENCE	323 AA;	36445 MW; 4DB8A90E9EIF4892 CRC64;
Query Match 21.9%; Score 219.5; DB 1; Length 323;			
Best Local Similarity 31.4%; Pred. No. 2.6e-11;			
Matches	44; Conservative	26; Mismatches	63; Indels 7; Gaps
<hr/>			
QY	37	NCPGEYSNDVCCKTCPSGTFFVKAPCKIPHTQGCEKCHPGT-FTGKDNLGHDCLEGST	95 : : : : : : : : : : : : : : : :
Db	44	SCQEGLYRHHQCFCPPGGKRKNKGCDKRDGDTPCVLCSENEYTDKSHHSDKCIRCSI	103 : : : : : : : : : : : : : : : :
QY	96	CDKDONVAD--CSATSDRKCECIGLYYYDPKPESCRCPTKCPQGIPIVLOECNSTANT	153 : : : : : : : : : : : : : : : : :
Db	104	CDEEHGLEVEQNCTRTNTKCRCKSN-PFCNSSPCEHCNPCTCBHGII-IETKTPTSNT	160 : : : : : : : : : : : : : : : :
QY	154	VCSSSVSNPRN-WLFLMLLI	172 : : : : : : : : : : : : : : : :
Db	161	KCKGRSRLANSLWALLILLI	180 : : : : : : : : : : : : : : : :
<hr/>			
RESULT 5			
TRIA_MOUSE			
ID	TRIA_MOUSE	STANDARD;	PRT; 454 AA.
AC	P25118;		
DT	01-MAY-1992 (Rel. 22, Created)		
DD	01-MAY-1992 (Rel. 22, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)		
DE	(TNF-R1) (TNF-R1) (p55).		
GN	TNFRSF1A OR TNFR1 OR TNFR-1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91l7885; PubMed=1849278;		
RA	Lewis M., Tartaglia L.A.; Lee A.; Bennett G.L.; Rice G.C.;		
RA	Wong G.H.; Chen E.Y.; Goeddel D.V.;		
RT	"Cloning and expression of cDNAs for two distinct murine tumor		
RT	necrosis factor receptors demonstrate one receptor is species		
RT	specific."		
KL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91246168; PubMed=1645445;		
RA	Goodwin R.G.; Anderson D.; Jerzy R.; Davis T.; Brannan C.I.;		
RA	Copeland N.G.; Jenkins N.A.; Smith C.A.;		
RT	"Molecular cloning and expression of the type 1 and type 2 murine		

QY 153 TVCS 156
Db 150 VVCS 153

RESULT 7

TRIA_RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91Y93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN=Various;
RA Furuya T., Salstrom J.L., Bina J., Hashimoto A., Dobbins D.E.,
Wildner R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
among autoimmune susceptible and resistant inbred rat strains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNF2/TNF-alpha and homotrimeric
TNF2/lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
signaling complex (DISC) performs caspase-8 proteolytic activation
which initiates the subsequent cascade of caspases (aspartate-
specific cysteine proteases) mediating apoptosis (by similarity).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC EMBL; M63122; AAA42256.1; -
CC EMBL; AF329976; AAK53562.1; -
CC EMBL; AF329977; AAK53563.1; -
CC EMBL; AF329981; AAK53567.1; -
CC EMBL; AF329978; AAK53564.1; -
CC EMBL; AF329979; AAK53565.1; -
CC EMBL; AF329980; AAK53566.1; -
CC PIR; B36555; B36555.
CC HSP; P19438; INCF.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; Death; 1.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 195
FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT VARIANT 230 230
FT VARIANT 295 295
FT SEQUENCE 461 AA; 50969 MW; EB33C05450FBD202 CRC64;
Query Match 21.0%; Score 210; DB 1; Length 461;
Best Local Similarity 27.4%; Pred. No. 2.1e-10;
Matches 52; Conservative 22; Mismatches 62; Indels 54; Gaps 7;
QY 38 CPDGEY---QSDNVCKTCPSGTFVAPCKIPHTQCEKCHPGTFTGKDNGLHDELCS 94
DB 44 CPQGYAHPKNNISICCTKCHGTLYLSDCPSPGOETVCEVCDKGTFTASQNHVROCLSK 103
QY 95 TCDDK--QNMVADCSATSDRKCEC---QIGLYYDPPKFPESCRCPTCKPQGIPLVQECNS 149
DB 104 TCRKMFQVEISPCKADMTVCCKKNQRYLSETHF--QCVDSPCFNG--TVTIPCKE 160
QY 150 TANTVCS-----SSVSNPRN-----WL 166
DB 161 KQTVNCNCHAGFLPSGNETPCSHCKKNQECMKLPPVAVNTNPQDSGTVALLPLVIFL 220
QY 167 FLMLLVFCI 176
DB 221 GLCLLFICFI 230
RESULT 8
ID CRMB_CAMPS
AC Q8UYA7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble TNF receptor II precursor (cytokine response modifying protein
DE B).
GN (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).


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Db 60 KTFQCPGSGTFSRNHLPACLSGRCNSNOVTRSCNTTHNRCECSPG-YCYLL 118
QY 126 KTFQCPGSGTFSRNHLPACLSGRCNSNOVTRSCNTTHNRCECSPG-YCYLL 118
Db 119 KGSQGRACVSTQKCGIGYVSGH-TSVGDVICS 151

RESULT 12
TRIA_BOVIN
ID TRIA_BOVIN STANDARD; PRT; 471 AA.
AC 019131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98273505; PubMed=9613449;
RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
  (TNF)-receptor 1.";
RL Vet. Immunol. Immunopathol. 61:379-385(1998).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
  TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
  caspase-8 to the activated receptor. The resulting death-inducing
  signaling complex (DISC) performs caspase-8 proteolytic activation
  which initiates the subsequent cascade of caspases (aspartate-
  specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
  HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
  PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
  WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
  PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
  TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
  ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
  NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U90937; AAB65143.1; -.
DR HSSP: P19438; 1TNR.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR Pfam: PF00531; death; 1.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR
  SUPERFAMILY MEMBER 1A.

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FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 233 POTENTIAL.
FT DOMAIN 234 471 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 195 TNFR-CYS 4.
FT DOMAIN 340 360 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 372 457 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 194 BY SIMILARITY.
FT DISULFID 185 190 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DFE81C4 CRC64;

Query Match 19.6%; Score 196; DB 1; Length 471;
Best Local Similarity 31.1%; Pred. No. 3e-09; Mismatches 63; Indels 32; Gaps 8;
Matches 51; Conservative 18;

QY 18 LLLNLFLPVIFA-----MP-----ESYFNCPDGEY---QSDNVCCCKTSPSGTFV 59
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 9 LLLPLVLPALLADVAGVQGLVPHPGDLEKRESPCPQKYNHPQNSTICCTKCHKGTYL 68
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 60 KAPCKIPHQGQCKHPGTFGKDNGLHDCLELCTCDKD--QNMVADCSATSDRKEC- 116
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 69 YNDCPGPRGDTDCRCAPGTATALENHLRRLCSRCRDEMFEQVEISPCVVDRTVCGCR 128
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY 117 --QIGLYYDVPKPSRCRCKPQG---IPVLOECNSTANTVC 155
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 129 KNOYREYWGTFG--RCLNCLCPNGTVNIP-----CQERQDTIC 166
  ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 13
TNFR6_RAT
ID TNFR6_RAT STANDARD; PRT; 324 AA.
AC Q63199;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
  receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
  (CD95)).
GN TNFRSF6 OR PT1 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94128114; PubMed=7507668;
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
  the rat liver.";
RL Biochem. Biophys. Res. Commun. 198:666-674(1994).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
  recruits caspase-8 to the activated receptor. The resulting death-
  inducing signaling complex (DISC) performs caspase-8 proteolytic
  activation which initiates the subsequent cascade of caspases
  (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
  mediated apoptosis may have a role in the induction of peripheral
  tolerance, in the antigen-stimulated suicide of mature T-cells, or

```


RT "The clinical spectrum in a large kindred with autoimmune
RT lymphoproliferative syndrome caused by a Fas mutation that impairs
RT lymphocyte apoptosis.";
RL J. Pediatr. 133:629-633(1998).
[14]
RN VARIANTS ALPS LYS-241 AND GLN-250.
RX MEDLINE=99192346; PubMed=10090885;
RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,
RA Straus S.E., Puck J.M.;
RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
RT influences penetrance.";
RL Am. J. Hum. Genet. 64:1002-1014(1999).
[15]
RN VARIANT ALPS GLY-272.
RX MEDLINE=99270228; PubMed=10340403;
RA Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,
RA Gahr M., Roessler J.;
RT "Defective apoptosis due to a point mutation in the death domain of
RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
RT lymphoma, and Hodgkin's disease.";
RL Exp. Hematol. 27:868-874(1999).
[16]
RN VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
RX MEDLINE=99126461; PubMed=9927496;
RA Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,
RA Elkon K.B.;
RT "The molecular basis for apoptotic defects in patients with CD95
RT (Fas/Apo-1) mutations.";
RL J. Clin. Invest. 103:355-363(1999).
[17]
RN VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
RX VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
RX MEDLINE=99005325; PubMed=9787134;
RA Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,
RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
RT extranodal disease and autoimmunity.";
RL Blood 92:3018-3024(1998).
[18]
RN VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
RX MEDLINE=21311411; PubMed=11418480;
RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
RA Roosen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
RA Fischer R.E., Jackson C.M., Lin A.Y., Baemler C., Siegfert E.,
RA Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
RT "The development of lymphomas in families with autoimmune
RT lymphoproliferative syndrome with germline Fas mutations and
RT defective lymphocyte apoptosis.";
RL Blood 98:194-200(2001).
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC Secreted (isoforms 2 to 6).
CC -!- ALTERNATIVE PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d,
CC 3/Del3/e, 4/b, 5/c and 6/TMDel/a; are produced by alternative
CC splicing.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS), also known as Canale-Smith
CC syndrome (CSS), a childhood syndrome involving hemolytic anemia
CC and thrombocytopenia with massive lymphadenopathy and
CC splenomegaly.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd95.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M67454; AAA63174.1; -;
DR EMBL; X63717; CAA45250.1; -;
DR EMBL; X89101; CAA61473.1; -;
DR EMBL; Z47993; CAA88031.1; -;
DR EMBL; Z47994; CAA88032.1; -;
DR EMBL; Z47995; CAA88033.1; -;
DR EMBL; Z70520; CAA94431.1; -;
Query Match 18.9%; Score 189.5; DB 1; Length 335;
Best Local Similarity 30.9%; Pred. No. 7.7e-09;
Matches 42; Conservative 19; Mismatches 68; Indels 7; Gaps 5;
QY 40 DGEVQSNVDCCKTCTPSGTFVKAPCKIPHTQGOCEKCHPG-TFTCKDNLGHLHDELCSTCDK 98
Db 50 EGUHHDGQFCHKPCPPGGERKARDCTVNGDEPDVPCQEGKEYTDKAHFSSKRCRLCDE 109
QY 99 DONNVAD--CSATSDRKCCEQIGLYYYDPKFPESCRCPTKCPQGPVQLQCNSTANTVCS 156
Db 110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSTNPKCK 166
QY 157 SSVSNPR-NWFLML 171
Db 167 EEGSRNLGWLCLLLL 182
Search completed: December 10, 2002, 15:06:15
Job time : 9.69136 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:03:51 ; Search time 28.7901 Seconds
(without alignments)
1259.609 Million cell updates/sec

Title: us-09-855-266a-1
Perfect score: 1000
Sequence: 1 MYTFSHVSLSHWFLLLLLL.....SSVSNPRNWLFLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvrius.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Match	Query %	Length	Description
1	288.5	28.8	438	13	Q9DFV0
2	250	25.0	357	13	Q9DF34
3	231	23.1	347	12	O57119
4	226	22.6	360	12	O57118
5	224.5	22.4	189	6	Q95185
6	222.5	22.2	446	6	Q95ND3
7	220.5	22.1	327	6	O97491
8	220	22.0	263	6	Q9XS60
9	220	22.0	320	6	Q9XS29
10	219	21.9	319	6	Q9FW79
11	217.5	21.8	351	12	O57121
12	213.5	21.3	189	6	O97530
13	213.5	21.3	349	12	O57305
14	211.5	21.1	348	12	O57103
15	211.5	21.1	348	12	O57108
16	211.5	21.1	348	12	O57277

17	211.5	21.1	349	12	O57101
18	211.5	21.1	349	12	O57102
19	211.5	21.1	349	12	O57291
20	211.5	21.1	351	12	O73559
21	209.5	20.9	326	12	O57120
22	208.5	20.8	349	12	O57098
23	208.5	20.8	349	12	O57099
24	208.5	20.8	349	12	O8UYA7
25	208.5	20.8	349	12	O57284
26	207.5	20.8	326	12	O57122
27	207.5	20.8	347	12	O57115
28	207.5	20.8	349	12	O57109
29	207.5	20.8	351	12	O57117
30	206.5	20.6	355	12	O85308
31	205.5	20.5	349	12	O57100
32	204	20.4	348	12	O57112
33	204	20.4	348	12	O85407
34	203	20.3	350	12	O57123
35	202.5	20.2	349	12	O57097
36	202.5	20.2	349	12	O57110
37	202.5	20.2	349	12	O57111
38	202.5	20.2	349	12	O89098
39	202.5	20.2	349	12	O89118
40	196.5	19.7	320	12	O57079
41	194	19.4	413	11	O99MM1
42	192.5	19.2	322	12	O72761
43	190.5	19.1	331	6	O9TSN4
44	190.5	19.1	331	6	O9BDN0
45	190.5	19.1	350	12	O57116

ALIGNMENTS

RESULT 1

ID	Q9DFV0	PRELIMINARY;	PRT;	438 AA.
AC	O9DFV0;			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Ovarian TNF receptor.			
GN	TNFRSFA.			
OS	Brachydanio rerio (Zebrafish) (Zebra danio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hobe J., Goetz F.W.;			
RT	"Molecular cloning and expression of a TNF receptor and two TNF			
RT	ligands in the fish ovary."			
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).			
DR	EMBL; AF250042; AAG24365.1;			
DR	HSSP; O14763; IDOG.			
DR	ZFIN; ZDB-GENE-010802-1; tnfrsfa.			
DR	InterPro; IPR000345; CytC_heme_bind.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00531; death; 1.			
DR	Pfam; PF00020; TNFR_c6; 3.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 3.			
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.			
DR	PROSITE; PS0017; DEATH_DOMAIN; 1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			
KW	Receptor.			
SQ	SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;			

Query Match 28.8%; Score 288.5; DB 13; Length 438;
Best Local Similarity 35.1%; Pred. No. 1.3e-23;


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SQ SEQUENCE 360 AA; 39370 MW; 3628AD87E4709378 CRC64;
Query Match 22.6%; Score 226; DB 12; Length 360;
Best Local Similarity 35.6%; Pred. No. 8.7e-17;
Matches 53; Conservative 21; Mismatches 67; Indels 8; Gaps 6;

QY 14 FLILLNLNLPVIFAMP-ESYSFNCPDGEYQSDVCKTCPSGTFVKAPC-KIPHTGQ 71
:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 YILLLLSCIIIIINSETPHEPSNGCKDNEYKHHHLACLCLCPPGTAYASRLCDKSTNTQ 63

QY 72 CEKCHPGTGTGKNGLDCELC-TCDDQNMVADCSATSDRKCECOIGLYYDPKFPES 130
:||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 CTSGSGTFTSRNHLPACLSCNGRCDNSQVETRSCNTHNRICECSPG-YCYLLKGGSG 122

QY 131 CRPC---TKCPQGIPTVLQECNSTANTVCS 156
: : ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 CKACVSTKCGMGVGVSGH-TPTGDVICS 150

RESULT 5
ID Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duthie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON-TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 22.4%; Score 224.5; DB 6; Length 189;
Best Local Similarity 34.4%; Pred. No. 6.7e-17;
Matches 53; Conservative 20; Mismatches 68; Indels 13; Gaps 6;

QY 15 LLLLLNLNLF-LPVIFAMP-----ESYSFNCPDGEY---QSDVCKTCPSGTFVKAPCKI 65
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 15 LLALLVEIPLRVTLGLPHLRDREKRAIPCQPGKYIHPQDNSICCTCKHKGTYLYNDCG 74

QY 66 PHTQGCCKCHPGTFTGKNGLDCELCSTCDKD--QNMVADCSATSDRKCECOIGLY-Y 122
: : ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 PGLDTCRECENGTFTASENYLRQCLSCSKRKEMYQVEISPTVYRDTVCGCRKNQYRY 134

QY 123 YDPKFESCRPCCTKCPQGIPTVLQECNSTANTVCS 156
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 YWSETHFOCLNCSLCLNG-TVQISCKETQNTVCT 167

RESULT 6
Q95ND3
ID Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tumour necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051103; BAB55455.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 22.2%; Score 222.5; DB 6; Length 446;
Best Local Similarity 34.4%; Pred. No. 2.6e-16;
Matches 53; Conservative 19; Mismatches 69; Indels 13; Gaps 6;

QY 15 LLLLLNLNLF-LPVIFAMP-----ESYSFNCPDGEY---QSDVCKTCPSGTFVKAPCKI 65
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 15 LLALLVEIPLRVTLGLPHLRDREKRAIPCQPGKYIHPQDNSICCTCKHKGTYLYNDCAG 74

QY 66 PHTQGCCKCHPGTFTGKNGLDCELCSTCDKD--QNMVADCSATSDRKCECOIGLY-Y 122
: : ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 PGLDTCRECENGTFTASENYLRQCLSCSKRKEMYQVEISPTVYRDTVCGCRKNQYRY 134

QY 123 YDPKFESCRPCCTKCPQGIPTVLQECNSTANTVCS 156
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 YWSETHFOCLNCSLCLNG-TVQISCKETQNTVCT 167

RESULT 7
O97491
ID O97491 PRELIMINARY; PRT; 327 AA.
AC O97491;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Fas protein.
GN FAS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
```



```
Best Local Similarity 31.5%; Pred. No. 4.6e-16;
Matches 56; Conservative 20; Mismatches 74; Indels 28; Gaps 7;

QY 13 WFLLLLLNLF-LPVIFAMPESYFNCPDGE-----YQSNVCCCKTSPGTFVKAP 62
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 5 WLLPLIL- - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY 63 CKIPHTQGOCEKCHPG-TFTGKNGHLHDCELCTCDKQNM--VADCSATSDRKCEQIG 119
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 58 CTSNEKPKCEPCQEGEYTDKSHFSKRCRCSILCDGEHGLEVEDTCTQNTKCRCKSN 117
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
QY 120 LYYIDPKFPESCPCPKCQGIPIVLEQCNSTANTVCSSSVSNPN-----WLFLLMLI 172
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 118 FFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKERGSGTTGSKHHLFWLSTLLLI 172

RESULT 11
O57121 PRELIMINARY; PRT; 351 AA.
AC O57121;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUNICH OPV89/4(CAT);
RX MEDLINE=20579014; PubMed=11136755;
RA Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT "Detection and differentiation of old world orthopoxviruses:
restriction fragment length polymorphism of the crmb gene region.";
RL J. Clin. Microbiol. 39:94-100(2001).
DR EMBL; U90232; AAB94388.1; -.
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 38394 MW; 6D0E4040C0E7F78 CRC64;

Query Match 21.8%; Score 217.5; DB 12; Length 351;
Best Local Similarity 36.3%; Pred. No. 7.4e-16;
Matches 53; Conservative 16; Mismatches 64; Indels 13; Gaps 6;

QY 22 LFLPVIF-----AMPESYFNCPDGEYQSNVCCCKTSPGTFVKAPC-KIPHTQGOCEK 74
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 10 LFLSCIIIRGVAPHEPGNGKDKNEYKHHLHLLCLSCPPTGYASRLDSKTNTTQCTS 69
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
QY 75 CHPGTFTGKNGHLHDCELCS-TCDDQNMVADCSATSDRKCEQIGLYYYDPKFPESCRC 133
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 70 CGSGFTSRNHLPAKLSNCRGDSNQVETRSCNTTHNRCESPG-YICLLKSGSGCKA 128
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
QY 134 C---TKCPQGIPIVLEQCNSTANTVCS 156
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 129 CVSQTKCGMGVGSQH-TSTGDVICS 153
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
O97530 PRELIMINARY; PRT; 189 AA.
AC O97530;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Canis familiaris (Dog).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21109092; PubMed=11182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSSP; P19438; ITNR.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER. 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 21.3%; Score 213.5; DB 6; Length 189;
Best Local Similarity 32.1%; Pred. No. 1.1e-15;
Matches 50; Conservative 20; Mismatches 69; Indels 17; Gaps 7;

QY 15 LLLLLLNLF-LPVIFAMPE-----SYFNCPDGEY---QSNVCCCKTSPGTFVKAPCKI 65
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 15 LLALLLEIYISVTALVPHPRNRVRAILCPQKGIHPQDDSICTCKHGTYLYNDCPG 74
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
QY 66 PHTGOCCEKCHPGTFTGKNGHLHDCELCTCDKQNMV--ADCSATSDRKCEC---QIGL 120
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 75 PGLDTDCRECENGTFTASENHLRQCLSCSKRKNQVEISPTVYRTVCCGRKNQYRF 134
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
QY 121 YYYDPKFPESCRCPTKCPQGIPIVLEQCNSTANTVCS 156
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 135 YWSETLF--QCNCNCSLCLNG-TVQISCOEKQNTICT 167
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
O57305 PRELIMINARY; PRT; 349 AA.
AC O57305;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUNICH OPV89/5(CAT), AND MUNICH OPV 91/1(CAT);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90233; AAB94389.1; -.
DR EMBL; U90228; AAB94384.1; -.
DR HSSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
SQ SEQUENCE 349 AA; 38063 MW; 424E08FDEDD04CF CRC64;

Query Match 21.3%; Score 213.5; DB 12; Length 349;
Best Local Similarity 31.6%; Pred. No. 2e-15;
Matches 56; Conservative 25; Mismatches 71; Indels 25; Gaps 8;
```

```
QY 14 FLALLLLNLFPLV--IFAMPESYSFNCNPDGEYQSNVDCVCKTSPGTFVFKAPC-KIPHTOG 70
Db 4 YILLLLSCIIINSIDTPHPSPNGCKNDNEYRHHLLCLCLSCPPGTYSRLCDSDKTNTWT 63
QY 71 QCEKCHPGTFTGKNGLDHCELCSS--TCDDQNNWVADCSATSRKCECQIGLYYYDPKFFE 129
Db 64 QCTPGSGTFTSRNNHLPACLSCNCRGDSNQVKTSCNTHNRICDCAPG--YYCLLKGS 122
QY 130 SCRPC---TKC-----PQGPVLOEC-----NSTANTV--CSSSVSNPRMWL 166
Db 123 GCKACVSTKCGIGYGVSGHTPTGDWCVSPCLGTYSHTVSSVDKCEPVPSNTFNI 179
RESULT 14
O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RC STRAIN=ZAIRE-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;
```

```
Query Match 21.1%; Score 211.5; DB 12; Length 348;
Best Local Similarity 39.0%; Pred. No. 3.4e-15;
Matches 48; Conservative 12; Mismatches 56; Indels 7; Gaps 5;

QY 38 CPDGEYQSNVDCVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKNGLDHCELCSS--TC 96
Db 32 CKDNEYRSRNLCLCLSCPPGTYSRLCD-SKNTQCTPCGSDTFTSHNNHLQAACLSNCRG 90
QY 97 DKDQNNWVADCSATSRKCECQIGLYYYDPKFFPESCRPC---TKCPQGPVLOECNSTANT 153
Db 91 DSNQVETRSCNTHNRICECPG--YYCLLKSGSGCRTCSKTKCGIGYGV-SGYTSTGDV 148
QY 154 VCS 156
Db 149 ICS 151
```

```
RESULT 15
O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
```

```
RN [1]
RC STRAIN=ZAIRE-1970;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 21.1%; Score 211.5; DB 12; Length 348;
Best Local Similarity 39.0%; Pred. No. 3.4e-15;
Matches 48; Conservative 12; Mismatches 56; Indels 7; Gaps 5;

QY 38 CPDGEYQSNVDCVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKNGLDHCELCSS--TC 96
Db 32 CKDNEYRSRNLCLCLSCPPGTYSRLCD-SKNTQCTPCGSDTFTSHNNHLQAACLSNCRG 90
QY 97 DKDQNNWVADCSATSRKCECQIGLYYYDPKFFPESCRPC---TKCPQGPVLOECNSTANT 153
Db 91 DSNQVETRSCNTHNRICECPG--YYCLLKSGSGCRTCSKTKCGIGYGV-SGYTSTGDV 148
QY 154 VCS 156
Db 149 ICS 151

Search completed: December 10, 2002, 15:07:15
Job time : 30.7901 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 14:56:26 ; Search time 29.2346 Seconds
(without alignments)
674.581 Million cell. updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSPNCPDGEYQSNV.....SSVSNPRNWLFLMLIVFCI 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	858	100.0	176	19 AAW80254	Amino acid sequenc
2	310	36.1	380	22 ABG09344	Novel human diagno
3	264.5	30.8	204	23 ABB81467	Murine TACH protei
4	209	24.4	461	11 AAR07450	Rat Tumour Necrosi
5	205	23.9	327	14 AAR41688	Murine Fas. Mus m
6	205	23.9	327	16 AAR78611	Murine Fas antigen
7	205	23.9	327	17 AAR92530	mFas sequence. Sy
8	205	23.9	327	20 AAW86241	Fas ligand (FasL)
9	205	23.9	327	21 AAB19344	Amino acid sequenc
10	204.5	23.8	285	18 AAW33359	TBP(20-190)/hcg-al

11	204.5	23.8	658	23	AAW49759	TNF-selectokine pr
12	200.5	23.4	139	22	AAW66977	Peptide: SEQ ID 12
13	200.5	23.4	154	21	AAW94711	Tumour necrosis fa
14	200.5	23.4	161	13	AAW27496	Native 30 kd TNF i
15	200.5	23.4	161	19	AAW59664	Human soluble tumo
16	200.5	23.4	161	19	AAW52267	Soluble tumour nec
17	200.5	23.4	161	20	AAW89233	Tumour necrosis in
18	200.5	23.4	161	22	AAW37676	Human 30 kDa TNF i
19	200.5	23.4	162	23	AAW48058	Human TNFRI extrac
20	200.5	23.4	168	13	AAW24084	Truncated TNF-alph
21	200.5	23.4	199	13	AAW24080	Truncated TNF-alph
22	200.5	23.4	211	20	AAW89225	Tumour necrosis fa
23	200.5	23.4	256	18	AAW33357	TBP(20-161)/hcg-al
24	200.5	23.4	280	18	AAW66979	Tnfr1 protein. Un
25	200.5	23.4	307	18	AAW33358	TBP(20-161)/hcg-be
26	200.5	23.4	309	16	AAW70108	TNF-R-GBPH fusion
27	200.5	23.4	311	20	AAW89229	Tumour necrosis fa
28	200.5	23.4	336	18	AAW33360	TBP(20-190)/hcg-be
29	200.5	23.4	349	22	AAW50523	Human tumour necro
30	200.5	23.4	366	20	AAW89228	Tumour necrosis fa
31	200.5	23.4	371	11	AAW07449	Tumour Necrosis Fa
32	200.5	23.4	397	20	AAW89227	Tumour necrosis fa
33	200.5	23.4	417	20	AAW89226	Tumour necrosis fa
34	200.5	23.4	420	20	AAW89224	Tumour necrosis fa
35	200.5	23.4	451	16	AAW70107	TNF-R-GBP 130 fusi
36	200.5	23.4	455	11	AAW07451	Human Tumour Necro
37	200.5	23.4	455	12	AAW10986	30kd TNF inhibitor
38	200.5	23.4	455	12	AAW11082	Human 55kd TNF-bin
39	200.5	23.4	455	13	AAW20787	TNF-alpha binding
40	200.5	23.4	455	13	AAW24000	TNF-alpha 55kd rec
41	200.5	23.4	455	14	AAW42059	Lambda derived TNF
42	200.5	23.4	455	16	AAW5084	p55 TNF-R. Homo s
43	200.5	23.4	455	20	AAW30934	Human tumour necro
44	200.5	23.4	455	21	AAW36266	Human tumour necro
45	200.5	23.4	455	21	AAW37800	Human tumour necro

ALIGNMENTS

RESULT 1
AAW80254
ID AAW80254 standard; Protein: 176 AA.
XX
AC AAW80254;
XX
DT 28-JAN-1999 (first entry)
XX
DE Amino acid sequence of protein 7F4.
XX
KW Protein 7F4; differentiation; osteoblast cell; bone growth;
bone sarcoma.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /note= "signal peptide"
FT Protein 29..176
FT Protein /note= "mature protein"
XX
PN WO9843998-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1998; 98WO-JP01511.
XX
PR 01-APR-1997; 97JP-0099653.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Kimura N, Toyoshima T;

DR WPI: 1998-568275/48.
XX N-PSDB; AAV68046.
PT Receptor protein inducing differentiation in osteoblast cells - has
PT extracellular region only and can be used for screening substances
PT for treatment of bone growth disorders
XX
XX
PS Claim 1; Pages 29-31; 51pp; Japanese.
XX
XX The present sequence represents a protein designated 7F4. This protein
CC is capable of inducing differentiation in osteoblast cells. The
CC protein may be used to screen compounds for the ability to bind to
CC it, for use as ligands, agonists or antagonists and inhibiting or
CC otherwise altering its differentiation inducing activity. Compounds
CC so identified, as well as the protein itself, DNA encoding it, and
CC antibodies to it, may be used in the treatment of diseases of bone
CC growth and osteoblast differentiation, such as bone sarcomas.
XX
SQ Sequence 176 AA;

Query Match 100.0%; Score 858; DB 19; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.6e-66;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCNPDGEYQSDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 29 AMPESYFNCNPDGEYQSDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 88
QY 61 DCELCSTCDKQNMVADCSATSDRKECQIGLYYYDPKFPESCRPCTKCPGIPVLQECN 120
DB 89 DCELCSTCDKQNMVADCSATSDRKECQIGLYYYDPKFPESCRPCTKCPGIPVLQECN 148
QY 121 STANTVCSYSSVSNRNMLFLMLLVFCI 148
DB 149 STANTVCSYSSVSNRNMLFLMLLVFCI 176

RESULT 2
ABG09344
ID ABG09344 standard; Protein; 380 AA.
XX
AC ABG09344;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9335.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI: 2001-639362/73.
DR N-PSDB; AAS73531.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX

PS Claim 20; SEQ ID No 39703; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 380 AA;

Query Match 36.1%; Score 310; DB 22; Length 380;
Best Local Similarity 77.1%; Pred. No. 8e-19;
Matches 54; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 AMPESYFNCNPDGEYQSDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 103 AMLELHSHFRCPAGEYKWDVCKCKNSAGTFVKAPCEIPHTQGCCKCHPGTFTGKDNGLH 162
QY 61 DCELCSTCDK 70
DB 163 ACILCSTCDK 172

RESULT 3
ABB81467
ID ABB81467 standard; Protein; 204 AA.
XX
AC ABB81467;
XX
DT 29-AUG-2002 (first entry)
XX
DE Murine TACH protein SEQ ID NO:2.
XX
KW TACH; tumour necrosis factor receptor family; TNF receptor; cancer;
KW inflammatory; immunoregulatory; cytostatic; antiinflammatory;
KW gene therapy.
XX
OS Mus sp.
XX
PN WO200228900-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30993.
XX
PR 04-OCT-2000; 2000US-237791P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOX-) APOXIS BIOSCIENCES LTD.
XX
PI Zheng T, Tschopp J, Schneider P;
XX
DR WPI: 2002-507878/54.
DR N-PSDB; ABN89334.
XX
PT Novel isolated tumor necrosis factor receptor family member nucleic
PT acid, termed TACH, useful for diagnosing, treating, preventing or

PT delaying cancer, inflammatory or immunoregulatory condition -
PS Claim 3; Fig 1; 87pp; English.

XX The present invention describes an isolated tumour necrosis factor (TNF)
CC receptor family member, designated TACH (I). (I) has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy. (I) can
CC be used for diagnosing, treating, preventing or delaying cancer, for
CC inflammatory or immunoregulatory conditions. (I) is also useful for
CC modulating the activity of cytokines, in screening assays, detection
CC assays (e.g. chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents murine TACH from the present invention.

XX Sequence 204 AA;

Query Match 30.8%; Score 264.5; DB 23; Length 204;
Best Local Similarity 37.6%; Pred. No. 3.4e-15;
Matches 47; Conservative 21; Mismatches 56; Indels 1; Gaps 1;

QY 10 CPDGEYQNDVCKTCPSGTFVKAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCCLCSTD 69
DB 27 CKIGEFKHENLCCLOCSAGTYLRNQCQENHNKSECAPCDSEHFDHKNRESECFPCSVCR 86
QY 70 KDQNMVADCSATSDRKCECQIGLYYDPPKFPESCRCPTKCPQGPVLCQECNSTANTVCSS 129
DB 87 DDQEEVAKSRTADVRCQCKGTYCDSENCLERCHTSCSPDG-RVVRKCNATMTDVTCDK 145
QY 130 SVSNP 134
DB 146 FDSEP 150

RESULT 4

AAR07450
ID AAR07450 standard; protein; 461 AA.

XX AAR07450;

XX 29-JAN-1991 (first entry)

DE Rat Tumour Necrosis Factor-Receptor from ratTNF-R8 CDNA.

XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW ratTNF-R8.

XX Rat rattus.

XX EP393438-A.

XX 24-OCT-1990.

XX 06-APR-1990; 90EP-0106624.

XX 21-JUN-1989; 89DE-3920282.

XX 21-APR-1989; 89DE-3913101.

XX (BOEH) BOEHRINGER INGELHEIMINT.

XX Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;

XX WPI; 1990-321987/43.

XX N-PSDB; AAQ06284.

XX DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanisms to TNF action

XX Disclosure; Fig 8(1-2); 51pp; German.

XX A rat brain cDNA analogue of the HS913T cDNA library from rat
CC glioma cell line C6 (ATCC CCL107) is prepared in lambda-gt11.

CC The isolated clone ratNF-R8 is used as probe to isolated the entire
CC human TNF receptor, as represented in AAQ06285.
CC See also AAQ06282-Q06285.

XX Sequence 461 AA;

Query Match 24.4%; Score 209; DB 11; Length 461;
Best Local Similarity 27.4%; Pred. No. 4.8e-10;
Matches 52; Conservative 22; Mismatches 62; Indels 54; Gaps 7;

QY 10 CPDGEY--QSDNVCKTCPSGTFVKAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCCLCS 66

DB 44 CPOGYAHKPNKNSICCTKCHKTYLVSDCPSGQETVCELSHKGTFTASQNHVROCLSK 103

QY 67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYDPPKFPESCRCPTKCPQGPVLCQECNS 121

DB 104 TCRKEMFQVEISPCRADMDTVCGCKKNQORYLSETHP--QCVDSPFCNG-TVTIPCKE 160

QY 122 TANTVCS-----SSVSNPRN-----WL 138

DB 161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCPLPPVANVTNPQDSGTAVLLPLVIFL 220

QY 139 FLLMLIVFCI 148

DB 221 GLCLLFFICI 230

RESULT 5

AAR41688

ID AAR41688 standard; Protein; 327 AA.

XX AAR41688;

XX 19-APR-1994 (first entry)

XX Murine Fas.

XX Murine; Fas; human; macrophage; cell strain; BAM3.

XX Mus musculus.

XX JP05219959-A.

XX 31-AUG-1993.

XX 14-FEB-1992; 92JP-0028090.

XX 14-FEB-1992; 92JP-0028090.

XX (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.

XX WPI; 1993-308326/39.

XX N-PSDB; AAQ48008.

XX DNA hybridising with sequence coding for human FAS protein - is
PT prepd. from e.g. BAM3 cell of mouse macrophage cell

XX Claim 1; Page 6-7; 8pp; Japanese.

XX This sequence represents the murine Fas protein. The cDNA encoding
CC this sequence hybridises with the human Fas gene and was isolated
CC from the mouse macrophage cell strain BAM3. This sequence may be
CC used for the production of large amounts of murine Fas.

XX Sequence 327 AA;

Query Match 23.9%; Score 205; DB 14; Length 327;

Best Local Similarity 31.5%; Pred. No. 7.4e-10;

Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

QY 9 NCPDGEYQSDNVCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDCCLCST 67

DB 43 NCSEGLYQGGPFCCQCPQCGKKKVEDCKRMNGGTPTCAPCTEGKEYMDKNHYADKRCRCL 102

```
Qy 68 CDKQNMVAD--CSATSDRKCEQIGLYYYDPKFPESCRCPTKCPQGIPLVLECNSTANT 125
Db 103 CDEHGLEVETNCTLTQNTKCKKCPD-FYCDSPGCEHCVRASCCEHG--TLEPCTATSNT 159

Qy 126 VCSSSVSNNRWLFLLMLIVFCI 148
Db 160 NCRK--QSPRNRLWLLTILVLLI 180

RESULT 6
AAR78611
ID AAR78611 standard; Protein; 327 AA.
XX
AC AAR78611;
XX
DF 19-FEB-1996 (first entry)
XX
DE Murine Fas antigen extracellular region.
XX
KW Murine Fas antigen; extracellular region; soluble membrane protein;
KW antibody production; diseases; treatment; prevention.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= sig_peptide
FT Peptide 22..327
FT /label= mat_peptide
XX
PN JP07115988-A.
XX
PD 09-MAY-1995.
XX
PF 26-OCT-1993; 93JP-0267644.
XX
PR 26-OCT-1993; 93JP-0267644.
XX
PA (NIBS ) JAPAN TOBACCO INC.
XX
WPI; 1995-202847/27.
DR N-PSDB; AAO95302.
XX
PT Preparation of soluble membrane proteins - for their use in antibody
PT production for the treatment and prevention of related diseases
XX
PS Example 2; Pages 32-33; 51pp; Japanese.
XX
CC AAQ95302 encodes AAR78611 the murine Fas antigen extracellular region.
CC The cDNA was used in the construction of an expression vector for
CC the prodn. of recombinant soluble membrane proteins. The proteins
CC can be used in antibody prodn. for the treatment and prevention of
CC related diseases.
XX
SQ Sequence 327 AA;
Query Match 23.9%; Score 205; DB 16; Length 327;
Best Local Similarity 31.5%; Pred. No. 7.4e-10;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

Qy 9 NCPDGEYSNDVCCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKONGLHDCELCST 67
Db 43 NCSEGLYOGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTL 102

Qy 68 CDKQNMVAD--CSATSDRKCEQIGLYYYDPKFPESCRCPTKCPQGIPLVLECNSTANT 125
Db 103 CDEHGLEVETNCTLTQNTKCKKCPD-FYCDSPGCEHCVRASCCEHG--TLEPCTATSNT 159

Qy 126 VCSSSVSNNRWLFLLMLIVFCI 148
Db 160 NCRK--QSPRNRLWLLTILVLLI 180
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RESULT 7
AAR92530
ID AAR92530 standard; Protein; 327 AA.
XX
AC AAR92530;
XX
DF 06-SEP-1996 (first entry)
XX
DE mFas sequence.
XX
KW Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..327
FT /note= "mature Fas"
FT Misc-difference 24
FT /note= "encoded by AGT"
XX
PN WO9601277-A1.
XX
PD 18-JAN-1996.
XX
PF 03-MAR-1995; 95WO-JP00349.
XX
PR 14-FEB-1995; 95JP-0025637.
PR 06-JUL-1994; 94JP-0154706.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA (NIBS ) JAPAN TOBACCO INC.
XX
PI Hachiya T, Noguchi J, Yonehara S;
XX
WPI; 1996-087635/09.
DR N-PSDB; AAT16305.
XX
PT Immunoassay method for soluble Fas antigen in body fluids - for
PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
PT systemic lupus erythematosus
XX
PS Example 9; Page 80-82; 124pp; Japanese.
XX
CC This sequence represents the mFas antigen used for the mFas.EXT,
CC contained within the plasmid pME18S. The soluble Fas antigen is included
CC in the immunoassay kit of the invention. The kit is for the assay of
CC soluble Fas antigen and contains an immobilised anti-soluble Fas
CC monoclonal antibody, as well as the standard soluble Fas antigen
CC represented by this sequence. The assay is simple and has high accuracy,
CC high sensitivity, and is capable of assaying a number of different
CC specimens at the same time. The immunoassay is used on biological
CC samples (such as serum) and is useful for diagnosis of autoimmune
CC diseases such as rheumatoid arthritis or systemic lupus erythematosus
CC (SLE).
```

SQ Sequence 327 AA;

Query Match 23.9%; Score 205; DB 17; Length 327;

Best Local Similarity 31.5%; Pred. No. 7.4e-10;

Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

Qy 9 NCPDGEYSNDVCCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKONGLHDCELCST 67

Db 43 NCSEGLYOGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTL 102

Qy 68 CDKQNMVAD--CSATSDRKCEQIGLYYYDPKFPESCRCPTKCPQGIPLVLECNSTANT 125

Db 103 CDEHGLEVETNCTLTQNTKCKKCPD-FYCDSPGCEHCVRASCCEHG--TLEPCTATSNT 159


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XX 19-MAR-1998 (first entry)
XX DE
XX TBP(20-190)/hCG-alpha fusion protein.
XX KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
XX KW alpha subunit; hCG-alpha.
XX OS Homo sapiens.
XX PN WO9730161-A1.
XX PD 21-AUG-1997.
XX PF 20-FEB-1997; 97WO-US02315.
XX PR 20-FEB-1996; 96US-0011936.
XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Campbell RK, Chappel SC, Jameson BA;
XX DR WPI: 1997-425036/39.
XX DR N-PSDB; AAT94021.
XX PT Hybrid dimeric protein comprising two co-expressed units - each
XX PT based on receptor or ligand and a subunit of a heterodimeric
XX PT hormone, especially FSH, for inducing follicular maturation
XX PS Example; Pages 37-38; 60pp; English.
XX CC A novel fusion protein comprises 2 dimer forming co-expressed amino
XX CC acid sequences, each consisting of a homodimeric or heterodimeric
XX CC receptor chain or ligand, with ligand-receptor binding activity,
XX CC bound directly or via a peptide linker to a subunit of a
XX CC heterodimeric protein hormone capable of forming a heterodimer with
XX CC the hormone's other subunits. The fusion protein, e.g. the
XX CC thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
XX CC (hCG-alpha) fusion protein denoted by the present sequence,
XX CC significantly increases the biological activity of the hormone
XX CC component, reducing the requirement for hormone itself and the
XX CC number of injections needed.
XX SQ Sequence 285 AA;
Query Match 23.8%; Score 204.5; DB 18; Length 285;
Best Local Similarity 34.4%; Pred. No. 7e-10;
Matches 43; Conservative 15; Mismatches 60; Indels 7; Gaps 4;
QY 10 CPDGEY---QSNDDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGDKDGLHDCCLCS 66
DQ 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 CPQCKYIHPONNSICTKCHKGTLYNDPCPGQDTDCRECSGFTASENHLRHCLSCS 85
QY 67 TCDKQDNV--ADCSATSDRKECOIGLY-YVDKFPESCRCPTKCPQGPVQLQECNSTA 123
DQ 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 KCRKEMGQVEISSCTVDRDTGCGCRKNQRYHWSENLFQCFNCTCLNG-TVHLSQCEKQ 144
QY 124 NTVCSS 128
DQ 145 NTVCT 149
RESULT 11
AAM49759
ID AAM49759 standard; Protein; 658 AA.
XX AC
XX AAM49759;
XX AC
XX 05-JUL-2002 (first entry)
XX DE TNF-selectokine produg W24.
XX KW Prodrug; W24; TNF; tumour necrosis factor; selectokine; chimeric;

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KW cytostatic; immunomodulatory; antiangiogenic; apoptosis inducer;
KW gene therapy; scfv antibody OS4; fibroblast activation protein;
KW solid tumour; angiogenesis; treatment; infection; metabolic disease.
XX OS Homo sapiens - Chimeric.
XX OS Gallus sp - Chimeric.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= leader_peptide
FT Region 20..285
FT /note= "scFv antibody OS4 specific for human
FT /note= fibroblast activation protein (FAP)"
FT Protein 20..658
FT /label= mature_W24
FT Domain 286..315
FT /note= "chicken tenascin trimerising domain"
FT Region 316..321
FT /note= "linker region"
FT Region 322..486
FT /note= "mutated form of human TNF precursor protein
FT (26 kDa membrane form) with a deletion in the
FT N-terminal region of the first 56 amino acids
FT and from aa78-89 (TNFdelta1-56,78-89), i.e. a
FT deletion in the cytoplasmic domain, the
FT transmembrane domain and the TACE cleavage
FT site"
FT Region 487..512
FT /note= "linker region with protease cleavage site"
FT Region 513..639
FT /note= "human TNFR1 fragment containing extracellular
FT domains 1-3"
FT Region 640..652
FT /note= "Myc-tag"
FT Region 653..658
FT /note= "His-tag"
XX WO200222833-A1.
XX 21-MAR-2002.
XX 17-SEP-2001; 2001WO-EP10730.
XX 15-SEP-2000; 2000DE-1045592.
XX (UYST-) UNIV STUTTGART.
XX (PFIZ/) PFIZENMAIER K.
XX Pfizenmaier K, Wuest T, Moosmayer D, Grell M, Scheurich P;
XX WPI: 2002-362351/39.
XX N-PSDB; ABA99913.
XX New polypeptide produg, useful e.g. for treating tumors, contains
XX targeting region, active agent and attached inhibitor that is
XX proteolytically cleaved in target cells -
XX Example 3; Fig 1; 52pp; German.
XX This invention describes a novel polypeptide (I) comprising, in the N
XX to C direction, a region (R1) that recognises selectively a specific
XX macromolecule on a cell surface and/or a component of the extracellular
XX matrix, peptide linker, a region (R2) with biological activity for a
XX specific target molecule, a region (R3) that has a processing site and a
XX region (R4) that inhibits the activity of R2, by intramolecular bonding
XX and/or interaction. The products of the invention have cytostatic,
XX immunomodulatory and antiangiogenic activity, induce apoptosis and can be
XX used for gene therapy. Kym-1 cells (20000) were incubated with the
XX produg W24, containing, essentially, the single-chain Fv antibody OS4,
XX specific for human fibroblast activation protein, trimerization linker,
XX mutant form of the tumour necrosis factor (TNF) precursor protein, a
XX region with a proteolytic cleavage site, and human TNF receptor-1
XX fragment, and with trypsin (activator) for 5 minutes. After 16 hours,

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OS Homo sapiens.
XX
PN WO9824463-A2.
XX
PD 11-JUN-1998.
XX
PF 08-DEC-1997; 97WO-US22733.
XX
PR 09-JUL-1997; 97US-0052023.
PR 06-DEC-1996; 96US-0032587.
PR 21-JAN-1997; 97US-0036355.
PR 07-FEB-1997; 97US-0039315.
XX
PA (AMGE-) AMGEN INC.
XX
PI Bendele AM, Edwards CK, Sennello RM;
XX
DR WPI; 1998-333039/29.
XX
DR N-PSDB; AAV41548.
XX
XX
PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
PT by administering tumour necrosis factor binding protein and at least
PT one additional anti-inflammatory drug, e.g. methotrexate
XX
PS Disclosure; Fig 1; 104pp; English.
XX
CC This is the amino acid sequence of the human tumour necrosis factor
CC receptor type I, used in the method of the invention involving the
CC treatment of acute or chronic inflammatory disease such as leukaemia
CC by administering tumour necrosis factor binding protein and at least
CC one additional anti-inflammatory drug, e.g. methotrexate.
XX
SQ Sequence 161 AA;

Query Match 23.4%; Score 200.5; DB 19; Length 161;
Best Local Similarity 33.6%; Pred. No. 8.5e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

QY 10 CPDGEY--OSNDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGFTTGKDNGLHDCCLCS 66
Db |||:| |:|:| | ||:| | | | | | | | | | | | | | | | |
4 CPOGKIYHPQNNISCCYKCHKGTLYNDPCPGQDTCRECESGSFTASENHLRHLCS 63

QY 67 TCDKQNMV--ADGSATSDRRKCEQIGLY-YYPKFPESCRCPTKCPGIPVLQECNSTA 123
Db | | : | : | : | | : | | : | | : | | : | | : | |
64 KCRKEMQVEISSCTVDBDFTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 122

QY 124 NTVCS 128
Db ||||:
123 NTVCT 127
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Search completed: December 10, 2002, 15:05:53
Job time : 30.2346 secs

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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:46 ; Search time 10.5062 Seconds
(without alignments)
414.479 Million cell updates/sec

Title: US-09-855-266A-2

Perfect score: 858

Sequence: 1 AMPESYFNCPPGEGYQSDV.....SSVSNPRNWLFLMLIVFCI 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	858	100.0	148	4	US-09-411-722-2
2	858	100.0	176	4	US-09-411-722-1
3	205	23.9	327	4	US-09-290-640-66
4	204.5	23.8	285	4	US-08-804-166-6
5	204.5	23.8	285	4	US-08-910-991-6
6	200.5	23.4	139	4	US-08-706-945D-129
7	200.5	23.4	153	2	US-08-219-237B-4
8	200.5	23.4	153	4	US-08-477-347-12
9	200.5	23.4	153	4	US-08-476-862-3
10	200.5	23.4	153	4	US-08-468-560C-4
11	200.5	23.4	154	4	US-08-828-683A-12
12	200.5	23.4	161	4	US-09-326-394-2
13	200.5	23.4	167	1	US-08-050-319B-2
14	200.5	23.4	167	1	US-08-050-319B-57
15	200.5	23.4	167	2	US-08-465-982-2
16	200.5	23.4	167	2	US-08-465-982-57
17	200.5	23.4	197	4	US-08-828-683A-21
18	200.5	23.4	256	4	US-08-804-166-2
19	200.5	23.4	256	4	US-08-910-991-2
20	200.5	23.4	280	3	US-08-974-022-46
21	200.5	23.4	280	4	US-08-795-445A-46
22	200.5	23.4	280	4	US-08-795-447A-46
23	200.5	23.4	280	4	US-08-974-186-46
24	200.5	23.4	280	4	US-08-795-446B-46
25	200.5	23.4	280	4	US-08-706-945D-132
26	200.5	23.4	307	4	US-08-804-166-4
27	200.5	23.4	307	4	US-08-910-991-4

28	200.5	23.4	336	4	US-08-804-166-8	Sequence 8, Appli
29	200.5	23.4	336	4	US-08-910-991-8	Sequence 8, Appli
30	200.5	23.4	349	4	US-09-006-353A-13	Sequence 13, Appl
31	200.5	23.4	349	4	US-09-573-986-13	Sequence 13, Appl
32	200.5	23.4	455	1	US-08-050-319B-25	Sequence 25, Appl
33	200.5	23.4	455	1	US-08-321-668-2	Sequence 2, Appli
34	200.5	23.4	455	1	US-08-837-941-2	Sequence 2, Appli
35	200.5	23.4	455	2	US-08-126-016-2	Sequence 2, Appli
36	200.5	23.4	455	2	US-08-465-982-25	Sequence 25, Appl
37	200.5	23.4	455	4	US-08-815-469-5	Sequence 5, Appli
38	200.5	23.4	455	4	US-09-006-353A-3	Sequence 3, Appli
39	200.5	23.4	455	4	US-09-527-236A-5	Sequence 5, Appli
40	200.5	23.4	455	4	US-08-054-970-2	Sequence 2, Appli
41	200.5	23.4	455	4	US-09-565-918-4	Sequence 4, Appli
42	200.5	23.4	455	4	US-09-573-986-3	Sequence 3, Appli
43	199.5	23.3	124	1	US-08-050-319B-4	Sequence 4, Appli
44	199.5	23.3	124	2	US-08-463-982-4	Sequence 4, Appli
45	199.5	23.3	199	1	US-08-050-319B-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-09-411-722-2

; Sequence 2, Application US/09411722

; Patent No. 6271366

; GENERAL INFORMATION:

; APPLICANT: Kimura, Naoki

; APPLICANT: Toyoshima, Tomoko

; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

; FILE REFERENCE: 06501/040001

; CURRENT APPLICATION NUMBER: US/09/411,722

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: PCT/JP98/01511

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: JP 9/099653

; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 148

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-411-722-2

Query Match 100.0%; Score 858; DB 4; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.2e-74;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMPESYFNCPPGEGYQSDVCKTCPSGTFVKAQKIPHTQGCCKCHPCTTGKDNGLH 60

Db 1 AMPESYFNCPPGEGYQSDVCKTCPSGTFVKAQKIPHTQGCCKCHPCTTGKDNGLH 60

Qy 61 DCELCSTCDKQNMVADCSATSDRKCEQIGLYYYDPKFPESCRCPTKCPQGPVLOECN 120

Db 61 DCELCSTCDKQNMVADCSATSDRKCEQIGLYYYDPKFPESCRCPTKCPQGPVLOECN 120

Qy 121 STANTVCSSVSNPRNWLFLMLIVFCI 148

Db 121 STANTVCSSVSNPRNWLFLMLIVFCI 148

RESULT 2

US-09-411-722-1

; Sequence 1, Application US/09411722

; Patent No. 6271366

; GENERAL INFORMATION:

; APPLICANT: Kimura, Naoki

; APPLICANT: Toyoshima, Tomoko

; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

; FILE REFERENCE: 06501/040001

; CURRENT APPLICATION NUMBER: US/09/411,722

; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match 100.0%; Score 858; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.4e-74;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCPCDGEYQSDVCKTSPGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 29 AMPESYFNCPCDGEYQSDVCKTSPGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 88
QY 61 DCELCSTCDKQNMVADCSATSDRCEQIGLYYDPPFPESCPCPKCPQGPVLOECN 120
DB 89 DCELCSTCDKQNMVADCSATSDRCEQIGLYYDPPFPESCPCPKCPQGPVLOECN 148
QY 121 STANTVCSSVSNPRNWLFLMLIVFCI 148
DB 149 STANTVCSSVSNPRNWLFLMLIVFCI 176

RESULT 3
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-290-640-66

Query Match 23.9%; Score 205; DB 4; Length 327;
Best Local Similarity 31.5%; Pred. No. 4e-12;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps 5;

QY 9 NCPDGEYQSDVCKTSPGTFVKAPCKIPHTQGCCKCHPG-TFTGKDNGLHDCELCST 67
DB 43 NCSEGLYGGPFCCQPCQPGKKGKVDCKMGNGTPTCAPCTEGKGYMDKNHYADKCRCTL 102
QY 68 CDKQNMVAD--CSATSDRCEQIGLYYDPPFPESCPCPKCPQGPVLOECNSTANT 125
DB 103 CDEEHGLEVEVETNCTLTQNTKCKKPD-FYCDSPGCEHCVCASCCEHG--TLEPCTATSN 159
QY 126 VCSVSSVSNPRNWLFLMLIVFCI 148
DB 160 NCRK--QSPRNLRLMLTILVLI 180

RESULT 4
US-08-804-166-6
; Sequence 6, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-804-166-6

Query Match 23.8%; Score 204.5; DB 4; Length 285;
Best Local Similarity 34.4%; Pred. No. 3.8e-12;
Matches 43; Conservative 15; Mismatches 60; Indels 7; Gaps 4;

QY 10 CPDGEY---QSDVCKTSPGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLHDCELCS 66
DB 26 CPQGYIHPQNNISICCTCKHGYLYNDPCPGQDTCDCESGSPASENHLRHCLSCS 85
QY 67 TCDKQNMV--ADCATSDRKCEQIGLY-YDPKFPESCPCPKCPQGPVLOECNSTA 123
DB 86 KCRKEMGQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQCFNCTCLNG-TVHLSQOEKQ 144
QY 124 NTVCS 128
DB 145 NTVCT 149

RESULT 5
US-08-910-991-6
; Sequence 6, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:05:57 ; Search time 6.85185 Seconds
(without alignments)
350.834 Million cell updates/sec

Title: US-09-855-266A-2

Perfect score: 858

Sequence: 1 AMPESYFNCPEYQSDV.....SSVSNPRNWLFLMLIVFCI 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	858	100.0	148	10	US-09-855-266A-2
2	858	100.0	176	10	US-09-855-266A-1
3	213.5	24.9	162	10	US-09-798-789-13
4	212.5	24.8	123	10	US-09-855-266A-13
5	209	24.4	461	9	US-09-898-234-15
6	209	24.4	461	9	US-09-899-429A-25
7	209	24.4	461	10	US-09-899-422-15
8	207.5	24.2	162	10	US-09-798-789-15
9	205	23.9	204	10	US-09-948-018-18
10	205	23.9	327	10	US-09-802-669-66
11	204.5	23.8	162	10	US-09-798-789-20
12	204.5	23.8	285	10	US-09-756-186-6
13	203.5	23.7	162	10	US-09-798-789-19
14	202.5	23.6	162	10	US-09-798-789-11
15	201.5	23.5	162	10	US-09-798-789-14
16	200.5	23.4	153	10	US-09-800-909-3
17	200.5	23.4	153	10	US-09-884-987-4
18	200.5	23.4	153	10	US-09-800-908-12
19	200.5	23.4	161	9	US-09-898-234-4

Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 20, Appli
Sequence 16, Appli
Sequence 10, Appli
Sequence 18, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
Sequence 17, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 27, Appli

20 200.5 23.4 161 9 US-09-899-429A-4
21 200.5 23.4 161 10 US-09-899-422-4
22 200.5 23.4 161 10 US-09-907-263-2
23 200.5 23.4 162 9 US-09-899-429A-6
24 200.5 23.4 162 10 US-09-798-789-9
25 200.5 23.4 162 10 US-09-798-789-21
26 200.5 23.4 162 10 US-09-798-789-22
27 200.5 23.4 172 9 US-09-899-429A-10
28 200.5 23.4 173 9 US-09-899-429A-16
29 200.5 23.4 183 9 US-09-899-429A-10
30 200.5 23.4 190 9 US-09-899-429A-18
31 200.5 23.4 200 9 US-09-899-429A-12
32 200.5 23.4 201 9 US-09-899-429A-14
33 200.5 23.4 211 9 US-09-899-429A-8
34 200.5 23.4 256 10 US-09-756-186-2
35 200.5 23.4 307 10 US-09-756-186-4
36 200.5 23.4 336 10 US-09-756-186-8
37 200.5 23.4 349 10 US-09-826-212-13
38 200.5 23.4 349 10 US-09-935-727-15
39 200.5 23.4 371 9 US-09-898-234-12
40 200.5 23.4 371 10 US-09-899-422-12
41 200.5 23.4 455 9 US-09-898-234-2
42 200.5 23.4 455 9 US-09-898-234-17
43 200.5 23.4 455 9 US-09-756-854-5
44 200.5 23.4 455 9 US-09-899-429A-2
45 200.5 23.4 455 9 US-09-899-429A-27

ALIGNMENTS

RESULT 1
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match 100.0%; Score 858; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.6e-64;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCPEYQSDVCCCKTCSGTFVKAPCKIPHTQGCCKCHPCTFTGKDNGLH 60
|||||
Db 1 AMPESYFNCPEYQSDVCCCKTCSGTFVKAPCKIPHTQGCCKCHPCTFTGKDNGLH 60
|||||
QY 61 DCELCSTCKDNQWVADCSATSDRKCECQIGLYYYDPKFPESCRCPTKCPQGPVLPQECN 120
|||||
Db 61 DCELCSTCKDNQWVADCSATSDRKCECQIGLYYYDPKFPESCRCPTKCPQGPVLPQECN 120
|||||
QY 121 STANTVCSSSVSNPRNWLFLMLIVFCI 148
|||||
Db 121 STANTVCSSSVSNPRNWLFLMLIVFCI 148
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US-09-855-266a-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266a-1

Query Match      100.0%; Score 858; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 5.4e-64;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCPCGVEQSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 1 AMPESYFNCPCGVEQSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
QY 29 AMPESYFNCPCGVEQSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLH 88
DB 29 AMPESYFNCPCGVEQSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLH 88
QY 61 DCELCSTCDKQNMWADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECN 120
DB 61 DCELCSTCDKQNMWADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECN 120
QY 89 DCELCSTCDKQNMWADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECN 148
DB 89 DCELCSTCDKQNMWADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECN 148
QY 121 STANTVCSSSVSNPRNWLFLMLIVFCI 148
DB 121 STANTVCSSSVSNPRNWLFLMLIVFCI 148
QY 149 STANTVCSSSVSNPRNWLFLMLIVFCI 176
DB 149 STANTVCSSSVSNPRNWLFLMLIVFCI 176

RESULT 3
US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahlyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-13

Query Match      24.9%; Score 213.5; DB 10; Length 162;
Best Local Similarity 35.2%; Pred. No. 3.4e-11;
Matches 44; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

QY 10 CPDGEY---QSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLHDELCS 66
DB 10 CPDGEY---QSNVDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLHDELCS 66

US-09-855-266a-13
; Sequence 13, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266a-13

Query Match      24.8%; Score 212.5; DB 10; Length 123;
Best Local Similarity 35.7%; Pred. No. 3.2e-11;
Matches 45; Conservative 13; Mismatches 57; Indels 11; Gaps 5;

QY 10 CPDGEY---OSNDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLHDELCS 66
DB 10 CPDGEY---OSNDVCKTSPGTFVFKAPCKIPHTQGCCKCHPGTFTGKDNGLHDELCS 66
QY 67 TCDKQNMW--ADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECNS 121
DB 67 TCDKQNMW--ADCSATSDRKECOIGLYYDVKPEPSCRCCTKCPQGIPIVLQECNS 121
QY 61 TCRKMSQVEISPCQADKDTVCCKENQFORLYSETHF--QCVDCSPFNG--TWTIPCKE 117
DB 61 TCRKMSQVEISPCQADKDTVCCKENQFORLYSETHF--QCVDCSPFNG--TWTIPCKE 117
QY 122 TANTVC 127
DB 122 TANTVC 127
QY 118 TQNTVC 123
DB 118 TQNTVC 123

RESULT 5
US-09-898-234-15
; Sequence 15, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
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; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-898-234-15

Query Match          24.4%   Score 209; DB 9; Length 461;
Best Local Similarity 27.4%; Pred. No. 2.le-10;
Matches 53; Conservative 22; Mismatches 62; Indels 54; Gaps 7;

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QY 67 TCDKXD--QNMVADCSATSDRKEC---QIGLYYYDPKFPESCRCCTKCPGIPVLOECNS 121
   |||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 104 TCRKEMFQVEISPCKADMDTVCGCKKQFORYLSETHF--QCVDPCSPFNG-TVTIPCKE 160

QY 122 TANTVCS-----SSVSNPRN-----WL 138
   |||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 161 KONTVCNCHAGFFLLSGNECTPCSHCKKQECMKLCLPPVANVTNPQDSGTAVLLPLVFL 220

QY 139 FLMLIVFCI 148
   | : | | |
Db 221 GLCLLFFICI 230

RESULT 6
US-09-899-429A-25
; Sequence 25, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-899-429A-25

Query Match          24.4%   Score 209; DB 9; Length 461;
Best Local Similarity 27.4%; Pred. No. 2.le-10;

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Matches	52:	Conservative	22:	Mismatches	62:	Indels	54:	Gaps	7:
Qy	10	CPDGEY----	QSNDCVCKTCPSGTFVKAPCKIPHHTQGOCCKCHPGCTFTGKDNGLHDCCLCS	66					
I	:		:		:		:		:
Db	44	CPOGKYAHPKNNSICCTKCHKGTLYLSDCSPSGOETVCELSHKGCTFTASONHHVRQCILSCK	103						
Qy	67	TCDDKD--QNMVADCSATSDRKEC---	QIGLYYYDPKFPPESCRCCTCKPQGIPIVLQECNS	121					
I	:		:		:		:		:
Db	104	TCREMFOVEISPCCKADMDTVCGCKKNQFORYLSETHF--QCVDCCSPCFNG-TVTIPCKE	160						
Qy	122	TANTVCS-----	SSVSNNPRN-----	WL	138				
I	:		:		:		:		:
Db	161	KONTVCNCHAGFFLSGNNECTPCSHCKKNQCEMKLCCLPPVANVTNPQDSGTAVLLPLVIFL	220						
Qy	139	FLLMLIVFCI	148						
I	:		:		:		:		:
Db	221	GLCLLFFICI	230						
RESULT 7									
US-09-899-422-15									
; Sequence 15, Application US/09899422									
; Patent No. US20020090676A1									
; GENERAL INFORMATION:									
; APPLICANT: Hauptmann, Rudolph									
; APPLICANT: Himmeler, Adolph									
; APPLICANT: Maurer-Foggy, Ingrid									
; APPLICANT: Stratowa, Christian									
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for									
; TITLE OF INVENTION: Them									
; FILE REFERENCE: 98.385-H									
; CURRENT APPLICATION NUMBER: US/09/899,422									
; CURRENT FILING DATE: 2001-08-21									
; PRIOR APPLICATION NUMBER: 09/525,998									
; PRIOR FILING DATE: 2000-03-15									
; PRIOR APPLICATION NUMBER: 08/383,676									
; PRIOR FILING DATE: 1995-02-01									
; PRIOR APPLICATION NUMBER: 08/153,287									
; PRIOR FILING DATE: 1993-11-17									
; PRIOR APPLICATION NUMBER: 07/821,750									
; PRIOR FILING DATE: 1992-01-02									
; PRIOR APPLICATION NUMBER: 07/511,430									
; PRIOR FILING DATE: 1990-04-20									
; NUMBER OF SEQ ID NOS: 87									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 15									
; LENGTH: 461									
; TYPE: PRT									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8									
US-09-899-422-15									
Query Match 24.4%; Score 209; DB 10; Length 461;									
Best Local Similarity 27.4%; Pred. No. 2.le-10;									
Matches	52:	Conservative	22:	Mismatches	62:	Indels	54:	Gaps	7:
Qy	10	CPDGEY----	QSNDCVCKTCPSGTFVKAPCKIPHHTQGOCCKCHPGCTFTGKDNGLHDCCLCS	66					
I	:		:		:		:		:
Db	44	CPOGKYAHPKNNSICCTKCHKGTLYLSDCSPSGOETVCELSHKGCTFTASONHHVRQCILSCK	103						
Qy	67	TCDDKD--QNMVADCSATSDRKEC---	QIGLYYYDPKFPPESCRCCTCKPQGIPIVLQECNS	121					
I	:		:		:		:		:
Db	104	TCREMFOVEISPCCKADMDTVCGCKKNQFORYLSETHF--QCVDCCSPCFNG-TVTIPCKE	160						
Qy	122	TANTVCS-----	SSVSNNPRN-----	WL	138				
I	:		:		:		:		:
Db	161	KONTVCNCHAGFFLSGNNECTPCSHCKKNQCEMKLCCLPPVANVTNPQDSGTAVLLPLVIFL	220						
Qy	139	FLLMLIVFCI	148						
I	:		:		:		:		:
Db	221	GLCLLFFICI	230						

Query Match	24.4%;	Score 209;	DB 9;	Length 461;
Best Local Similarity	27.4%;	Pred. No. 2.1e-10;		


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Query Match      23.8%; Score 204.5; DB 10; Length 162;
Best Local Similarity 33.6%; Pred. No. 1.9e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps

QY    10 CPDGEY---QSNDVCCKTSPSGTFVKAACKIPHTGQCCEKCHPGTTFGKDNGLHDCLEICS 66
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     5 CPOGKYIHPQNNSICTCKCHKGTLYLNDPCPGQDDTCRECESGSFTASENHLRHCLSCS 64
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    67 TCDKQDNW--ADCSATSDRKRCBCQIGLY-YYPDKFPESCRCPTKCPGPIPVLOECNSTA 123
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     65 KCRKEMGQVEISCTVDRTDFVCCRRKNQRHYOSENLFQCFNCSLCLNG-TVHLSCOEQK 123
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    124 NTVCS 128
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB     124 NTVCT 128
       |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
US-09-756-186-6
; Sequence 6, Application US/09756186
; Patent No. US2001001433A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-186-6

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	Query Match	23.8%	Score	204.5;	DB	10;	Length	285;
	Best Local Similarity	34.4%;	Pred.	No. 3.le-10;				
	Matches	43; Conservative	15; Mismatches	60; Indels	7; Gaps	4;		
QY	10 CPGEY--OSNDVCKTCSGTFVKAPCKIPHTQGCEKCHPCFTFGKNGLHDCELCS	66 : :	: :	:	: :	:	:	:
Dd	26 CPGKYTHPNNSICCTFKHKGTLYLWDCPGGDTPCRECESGSFASENHLRHCUSCS	85 : :	: :	:	: :	:	:	:
QY	67 TCDKDQNHW--ADCSATSDRKCECIGLY-YYPDFFPESCRPTCKCPGPIPVLECNSTA	123 : :	: :	:	: :	:	:	:

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Db      86 KCRKEMQVFISSCTVDRTVCGRKNQYRHYHSENLFCFENCTLCING-TVHLSQBEKQ 144
Qy      124 NTWCS 128
      ||||:
Db      145 NTVCT 149

RESULT 13
US-09-798-789-19
; Sequence 19, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-19

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[illegible]

```

RESULT 14
US-09-798-789-11
; Sequence 11, Application US/09798789
; Patent No. US2002009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798, 789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-11

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:21 ; Search time 13.2469 Seconds
(without alignments)
1074.054 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYFNCPDGEYQSDV.....SSVSNPRNWLFLMLIVFCI 148
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215.5	25.1	454	1 GOMST1	tumor necrosis fac
2	210	24.5	461	1 GQRTT1	tumor necrosis fac
3	205	23.9	327	2 A46484	apoptosis-mediati
4	200.5	23.4	348	2 T28623	hypothetical prote
5	200.5	23.4	349	2 D72175	G2R protein - vari
6	200.5	23.4	349	2 D36858	gene G4R protein -
7	200.5	23.4	455	1 GQHUT1	tumor necrosis fac
8	193.5	22.6	461	2 JC4302	tumor necrosis fac
9	190	22.1	324	2 JC2395	Fas antigen precu
10	189.5	22.1	335	2 A40036	apoptosis-mediati
11	177.5	20.7	427	1 GQHUN	nerve growth facto
12	177	20.6	314	2 I37383	FAS soluble protei
13	177	20.6	651	2 JC7705	death receptor-6 -
14	168.5	19.6	425	1 A26431	nerve growth facto
15	164.5	19.2	326	1 GQVZML	T2 protein - myxom
16	163.5	19.1	416	2 B43692	nerve growth facto
17	156	18.2	325	2 B43692	T2 protein - rabbi
18	148.5	17.3	461	1 A35356	tumor necrosis fac
19	148	17.2	250	1 A49053	CD27 antigen precu
20	146	17.0	435	2 I54182	tumor necrosis fac
21	144.5	16.8	474	2 B38634	tumor necrosis fac
22	143.5	16.7	260	1 A46517	CD27 antigen precu
23	143	16.7	271	2 SI2783	OX40 antigen precu
24	142.5	16.6	459	2 I48854	gene murine tumour
25	138	16.1	595	2 A42086	CD30 antigen precu
26	136.5	15.9	1790	1 MMFFB1	laminin beta-1 cha
27	135.5	15.8	493	2 JC5486	membrane glycoprot
28	134	15.6	277	2 I37552	OX40 homolog - hum
29	134	15.6	305	2 A46476	B cell-associated

RESULT 1

GOMST1

tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; I54532; I57826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO2>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissnerghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014; PMID:1647956
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815; PMID:1657766
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F. Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A:Reference number: I54532; MUID:94245292; PMID:8188324
A:Accession: I54532
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: GB:I26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R:Rothe, J.G.; Bluthmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis fact
A:Reference number: I57826; MUID:93156721; PMID:8381516

ALIGNMENTS

30	130	15.2	256	2	B32393	T-cell antigen 4-1
31	126.5	14.7	1193	2	A44018	laminin B2t chain
32	125.5	14.6	1192	2	S69000	laminin gamma 2 ch
33	124	14.5	1827	2	T34288	hypothetical prote
34	123.5	14.4	255	2	I38426	lymphocyte activat
35	122	14.2	272	2	I48700	gene ox40 protein
36	122	14.2	435	2	S40993	hypothetical prote
37	121.5	14.2	1274	2	T42017	cysteine rich prot
38	120	14.0	4391	2	A38096	perlecan precursor
39	119.5	13.9	1609	1	MMHUB2	laminin gamma-1 ch
40	118	13.8	570	2	T37314	probable kexin (EC
41	118	13.8	942	2	D87803	protein bli-4D (im
42	117	13.6	1548	2	S34583	serine proteinase
43	116	13.5	557	2	A48434	variant-specific s
44	115.5	13.5	1372	2	T25933	hypothetical prote
45	115.5	13.5	1808	2	T15099	hypothetical prote

A:Accession: I57826
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-393,'G','395-454 <RED>
A:CROSS-references: GB:W76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and tumor necrosis factor receptor.
C:Genetics:
A:Gene: TNFR-2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
E:1-29/Domain: signal sequence #status predicted <SIG>
E:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-212/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
E:213-235/Domain: transmembrane status predicted <MEM>
F:236-454/Domain: intracellular status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.1%; Score 215.5; DB 1; Length 454;
Best Local Similarity 28.1%; Pred No. 1.2e+09;
Matches 52; Conservative 23; Mismatches 61; Indels 49; Gaps 7;

Oy 10 CPDGEY---QSDNVCKTCPSGTFTVKA PKIPHTQGQCCKHPGTTFKDNGLHDCELCS 66
|| || : | : | : || | : | : | : | : | : | : |
Db 44 CPOKKGVHSKNNSICTCTKHKTGYLVSDCPSPGRDTVCRECEKGTTASQNVLRLQLSLCK 103
| : | : | : | : | : | : | : | : | : | : | : | : |

Oy 67 TCDDONMV--ADCSATSDRKCEC---QIGLYYYDPKPFPESCRPTCKPQQGPVPLQEENS 121
|| || : | : | : | : | : | : | : | : | : | : |
Db 104 TCRKEMSQVEISPCQAOKDVTCGCCKENOFQRYLSETHF--OCVDSCSPCFNG-TVTTPCKE 160
| : | : | : | : | : | : | : | : | : | : | : | : |

Oy 122 TANTVCGS-----SSVSNPNN-----WLFLML 143
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 161 TONTVCNHAGFFLRSECVPCSHCKNECMKLCLPPPLANVTNPQDSSTAVLLPLVIL 220
| : | : | : | : | : | : | : | : | : | : | : | : |

Oy 144 IVFCI 148
| : | : | : | : | : | : | : | : | : | : | : | : |
Db 221 LGLCL 225
| : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 2
GORTL1
tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C:Accession: B36555
R:Hummier, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A>Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <XIM>
A:CROSS-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and tumor necrosis factor receptor.
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
E:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:30-201/Product: tumor necrosis factor binding protein
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane status predicted <MEM>
F:235-461/Domain: intracellular status predicted <INT>
F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	24.5%;	Score 210;	DB 1;	Length 461;	
Best Local Similarity	27.4%;	Pred. No. 3.2e-09;			
Matches	52;	Conservative	22;	Mismatches	62;
				Indels	54;
				Gaps	7;

Qy	10	CPDGEY--OSNDVCKTCPSGTFVKAPCKIPHTQGOCEKCHPGFTTCKDNGLHDCELCS	66
Db	44	CPQGYAHPKNNSICCTCKHKGTYLVSDCPSPGQETVCEVCKDGTFTASQNNHVROCLSK	103
Qy	67	TCDDKD--QNNVADCSATSDRKCEC---QIGLYYYDKFPESCRCPTCKPQGIPIVLQECNS	121
Db	104	TCRKEMFQVEISPCAKADMTVCCGCKNQFORYLSETHF--QCVDSCSPFNG--TVTIPCKE	160
Qy	122	TANTVCS-----SSVSNPRN-----WL	138
Db	161	KQNTVCNCHAGFLSGNNECTPCSCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL	220
Qy	139	FLLLMLIVFCI	148
Db	221	GLCLLFFICI	230

RESULT	3
A46484	apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species:	Mus musculus (house mouse)
C:Date:	18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession:	A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki	
J. Immunol.	148, 1274-1279, 1992
A:Title:	The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A:Reference number:	A46484; MUID:92148151; PMID:1371136
A:Accession:	A46484
A:Status:	preliminary
A:Molecule type:	mRNA
A:Residues:	1-327 <WAT>
A:Cross-references:	GB:M83649; NID:gl93225; PIDN:AAA37593.1; PID:gl93226
A:Experimental source:	BAM3 macrophage cell line
A:Note:	sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.	
Proc. Natl. Acad. Sci. U.S.A.	90, 1756-1760, 1993
A:Title:	Aberrant transcription caused by the insertion of an early transposable elem
A:Reference number:	A47254; MUID:93189576; PMID:7680478
A:Accession:	A47254
A:Status:	preliminary
A:Molecule type:	nucleic acid
A:Residues:	1-96 <ADA>
A:Cross-references:	GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Experimental source:	MRL lpr/lpr
A:Note:	sequence extracted from NCBI backbone
C:Superfamily:	NGF receptor repeat homology
C:Keywords:	transmembrane protein
F:44-79/Domain:	NGF receptor repeat homology <NGF>
F:81-124/Domain:	NGF receptor repeat homology <NG4>

Query Match	23.9%;	Score 205;	DB 2;	Length 327;	
Best Local Similarity	31.5%;	Pred. No. 6.1e-09;			
Matches	45;	Conservative	23;	Mismatches	67;
				Indels	8;
				Gaps	5;

Qy	9	NCPDGEYQNDVCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDCELCST	67
Db	43	NCSEGLYQGGPFCCQPCQCPQCKKVEDCKMNGGTPTCAPCTEGKEYMDKNHVAADRCRRCTL	102
Qy	68	CDKQDNWVAD--CSATSDRKCEQIGLYYYDYPKFPESCRCPTCKPQGIPIVLQECNSTANT	125
Db	103	CDEHGLEVTNCTLLQNTKCKCKPD-FYCDSPGCEHCVCASCSEHG--TLEPCTATSNAT	159
Qy	126	VCSSSVSNPRNWLFLMLIVFCI	148
Db	160	NCRK--QSPNRNMLTILVILL	180

RESULT	4
T28623	

hypothetical protein G2R - variola major virus
C:Species: variola major virus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T28623
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A>Title: Potential virulence determinants in terminal regions of variola smallpox virus A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 23.4%; Score 200.5; DB 2; Length 348;
Best Local Similarity 36.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 16; Mismatches 55; Indels 7; Gaps 5;

QY 10 CPDGEVQSNDVCKTCPSGTFVKAPCKIPHTQGOCERKHPGTFTGKDNLHDCCLCS-TC 68
| | | : : : || : | | | | | | | | | : |
Db 31 CKDTEYKRHNLCCLSCPPGYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPAQLSCNGRC 89
| | | : : : || : | | | | | | | | | : |

QY 69 DKDQNWADCSATSKRKCEQIGLYYYDPKPESCRPC---TKCPQGIPIVLQECNSTANT 125
: | : | : | | | | | | : | | | | : |
Db 90 NSNQVETRSCNTHNRICECSPG-YVCLLKGGSSGCKACVSQTCKGIGYGVS GH-TSVGDV 147

QY 126 VCS 128
: ||
Db 148 ICS 150
: ||

RESULT 5
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutarov, V.V.; Safronov, P.F.; Massung, R.F.; Lopat submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 23.4%; Score 200.5; DB 2; Length 349;
Best Local Similarity 36.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 16; Mismatches 55; Indels 7; Gaps 5;

QY 10 CPDGEVQSNDVCKTCPSGTFVKAPCKIPHTQGOCERKHPGTFTGKDNLHDCCLCS-TC 68
| | | : : : || : | | | | | | | | | : |
Db 32 CKDTEYKRHNLCCLSCPPGYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPAQLSCNGRC 90
| | | : : : || : | | | | | | | | | : |

QY 69 DKDQNWADCSATSKRKCEQIGLYYYDPKPESCRPC---TKCPQGIPIVLQECNSTANT 125
: | : | : | | | | | | : | | | | : |
Db 91 NSNQVETRSCNTHNRICECSPG-YVCLLKGGSSGCKACVSQTCKGIGYGVS GH-TSVGDV 148

QY 126 VCS 128
: ||
Db 149 ICS 151
: ||

RESULT 6
D36858
gene G4R protein - variola virus

A>Title: Isolation and characterization of a tumor necrosis factor binding protein fr
A:Reference number: A60594; MUID:89171156; PMID:2924890

A:Accession: A60594

A:Molecule type: protein

A:Residues: 41-43,'X','Y',55-57,'XK',60 <OLS>

A:Experimental source: renal failure patient urine

R:Engelmann, H.; Novick, D.; Wallach, D.

J Biol Chem. 265, 1531-1536, 1990

A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden

A:Reference number: A35010; MUID:90110215; PMID:2153136

A:Accession: A35010

A:Molecule type: protein

A:Residues: 41-45 <ENG>

A:Experimental source: normal urine

R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.

Biosci Biotechnol Biochem 58, 2266-2268, 1994

A>Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purifie

A:Reference number: JC2404; MUID:95128033; PMID:7765720

A:Accession: JC2404

A:Molecule type: protein

A:Residues: 41-53,'X','Y',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>

A:Experimental source: urine

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)

C:Genetics:

A:Gene: GDB:TNFRI

A:Cross-references: GDB:125913; OMIM:191190

A:Map position: l2pl3.2-l2pl3.2

A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>

F:30-211/Domain: extracellular #status predicted <EXT>

F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat

F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-196/Domain: NGF receptor repeat homology <NG4>

F:212-234/Domain: transmembrane #status predicted <MEM>

F:235-455/Domain: intracellular #status predicted <INT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
C:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      22.6%; Score 193.5; DB 2; Length 461;
Best Local Similarity 32.3%; Pred. No. 6e-08;
Matches 41; Conservative 17; Mismatches 58; Indels 11; Gaps 5;

QY 10 CPDGEY---QSNVCCCTCPSGTFVKAPKIPHTQGOCEKCHPGFTGKDNGLHDXELCS 66
||| ||| | : ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44 CPQKYSHPNRSCCTCKCHKGTLYHNDCLGPGDLTDRCEDNGTFTASENHLTQCLSCS 103
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 67 TCDKQNMV---ADGSATSDRRKEC---QIGLYYYDPKFPESCRCPTKCPQGIPLVQECNS 121
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 104 KCRSEMSEVSPCTVDRDTCVGCGRKNQYKYSWSETLF--QCLNCSLCPNG-TVQLPCLE 160
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 122 TANTVCS 128
: ||| :
Db 161 KQDTICN 167
: ||| :

RESULT 9
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <IM>
A:Cross-references: DDBJ:D26112; NID:g468486; PIDN:BA005108.1; PID:d1005650; PID:g468487
A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RPT' <K12>
A:Cross-references: DDBJ:D26113; NID:g468488; PIDN:BA005109.1; PID:d1005651; PID:g468489
A:Experimental source: liver
C:Genetics:
A:Introns: 62/1
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <MAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>

Query Match      22.1%; Score 190; DB 2; Length 324;
Best Local Similarity 30.7%; Pred. No. 8.7e-08;
Matches 46; Conservative 22; Mismatches 64; Indels 18; Gaps 8;

QY 9 NCPDGEYQSNVCCCTCPSGTFVKAPKIPHTQGOCEKCHPGT---FTGKDNGLHDXCEL 64
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 NCSEGLYQVGFCCQCPQCPQKVKYKDT---TSGAPTCHPCTEGEYTRKHYSKRCRR 99
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 65 CSTCDKDONWAD--CSATSDRKCECQIGLYYYDPKFPESCRCPTKCPQGI-PVLQECNS 121
```

```
||| ||| : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 100 CAPCDEGHGLEVEETNCTRTQNTKCRCKEN-FYCNASLCHDCHYCTSC--GLEDILEPCTR 156
QY 122 TANTVCSVSNSPR-NWLFLL----MLIVF 146
| : | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 157 TSNTKCKKQSSNKKLLWLLILPLGLAILFVF 186

RESULT 10
A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C:Accession: A40036; S24543; A38142
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Ha;
Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITO>
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410.
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; R;
J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a memb
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'O', 136-335 <OEH>
A:Experimental source: SKW6.4 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)
C:Genetics:
A:Gene: GDB:APL1
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: NGF receptor repeat homology
C:Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4>
F;174-190/Domain: transmembrane #status predicted <TMM>

Query Match      22.1%; Score 189.5; DB 2; Length 335;
Best Local Similarity 30.9%; Pred. No. 9.8e-08;
Matches 42; Conservative 19; Mismatches 68; Indels 7; Gaps 5;

QY 12 DGEYQSNVCCCTCPSGTFVKAPKIPHTQGOCEKCHPG-TFTGKDNGLHDXELCSTCK 70
| : | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 50 EGLHHDGQFCHKPCPPGKERKARDCTVNGDEPCVPCQEGKEYTDKRAHFSKRCRRCLCDE 109
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 71 DONWAD--CSATSDRKCECQIGLYYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCS 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCBHGI--IKECLTTSNTCK 166
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 129 SSVNSPR-NWLFLLML 143
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 167 EEGSRSLNGLWLCILLLL 182
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
GOHUN
nerve growth factor receptor precursor, low affinity [validated] - human
```

RESULT 12

I37383
FAS soluble protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I37383
R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule
A:Reference number: I37383; MUID:95181785; PMID:7533181
A:Accession: I37383
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-314 <RES>
A:Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539

Query Match 20.6%; Score 177; DB 2; Length 314;
Best Local Similarity 30.1%; Pred. No. 8.6e-07;
Matches 37; Conservative 18; Mismatches 62; Indels 6; Gaps 4;

QY 12 DGEYSNDVCCCKTSPSGTFVKAPCKIPHTGOCCEKCHPG-TFTGKDGLHDCELCSTCDK 70
: : | : | | | : : : : : : : : : : : : | : | :
Db 50 EGLHHGDGFCHKPCPGBERKARDCIVNGDEPDVCQEGKEYTDKAHFSSKRCRRCLDCE 109
:
QY 71 DONMVA--CSATSDRKCECOIGLYYPKPFPESCRCPTCKPOGPVLQECNSTANTVCS 128
: : : : : : | : | : : : : : : : : : : : : : : :
Db 110 GHGLEVEINCTRTQTNTKCRCPN-PFCNSTVCEHCDCPTCKEHGI--IKECTLTSNTKCK 166
:
QY 129 SSV 131
|
Db 167 EEV 169

RESULT 13
JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7705
R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705; MUID:21308433; PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNFR family and activates a cell death and/or survival signaling cascade.
C:Genetics:
A:Gene: dr-6
C:Keywords: ovary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F:332-350/Domain: transmembrane #status predicted <TM>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.6%; Score 177; DB 2; Length 651;
Best Local Similarity 29.8%; Pred. No. 1.4e-06;
Matches 39; Conservative 22; Mismatches 58; Indels 12; Gaps 4;

[illegible]

RESULT 14

A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R:Metzlis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic acid.
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells.
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of the binding site.
C:Comment: This protein is thought to form a high-affinity receptor when it associates with p75.
C:Genetics: 20/3
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine kinase
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.6%; Score 168.5; DB 1; Length 425;
Best Local Similarity 32.8%; Pred. No. 4.8e-06;
Matches 39; Conservative 10; Mismatches 65; Indels 5; Gaps 3;

QY 10 CPDGEYQSNVDCCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDLCELCSTC 68
DB 33 CSTGLYTHSGECKACNLGEGVAQPCGA--NQTVCEPCLDNVTFSDVVVATEPCPKCTEC 90
QY 69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQIGIPVLQECNSTANTVC 127
DB 91 LGLQSNAPCVCEADDAVRCAYG--YYQDEETGHCEACSVCEVSGGLVFCQDKQNTVC 147

RESULT 15

GVQZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor.
A:Reference number: A40566; MUID:91335768; PMID:1651597
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein

F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2%; Score 164.5; DB 1; Length 326;
Best Local Similarity 31.7%; Pred. No. 8.1e-06;
Matches 39; Conservative 13; Mismatches 64; Indels 7; Gaps 5;
QY 10 CPDGEYQSNVDCCKTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDLCELC-STC 68
DB 28 CRGNDYKDGGLCTSCPPGSGYASRLCG-PGSDTVCSCKNETFTTASTNHAPACVSGRGRC 86
QY 69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQIGIPVLQECNSTANT 125
DB 87 TGHLSQSQCDKTRDRVDCSAGNYCL-LKGOEGCRICAPKTKCPAGYGVSGH-TFTGDV 144
QY 126 VCS 128
DB 145 LCT 147

Search completed: December 10, 2002, 15:07:52
Job time : 14.2469 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 14:57:06 ; Search time 7.30864 Seconds
(without alignments)
839.896 Million cell updates/sec

Title: US-09-855-266A-2

Perfect score: .858

Sequence: 1 AMPESYFNCPDGEYQSDV.....SSVSNPRNWLFLMLIVFCI 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	858	100.0	176	1	TR23_MOUSE
2	641	74.7	180	1	Q9er63 mus musculu
3	226.5	26.4	332	1	TR22_MOUSE
4	219.5	25.6	323	1	TNR6_PIG
5	215.5	25.1	454	1	P51867 bos taurus
6	211.5	24.7	351	1	TR1A_MOUSE
7	210	24.5	461	1	CRMB_COMPX
8	208.5	24.3	349	1	TR1A_RAT
9	205	23.9	327	1	CRMB_CAMPS
10	200.5	23.4	349	1	TNR6_MOUSE
11	200.5	23.4	455	1	CRMB_VARV
12	193.5	22.6	461	1	TR1A_HUMAN
13	190	22.1	324	1	TR1A_PIG
14	189.5	22.1	335	1	TNR6_RAT
15	186.5	21.7	471	1	TNR6_HUMAN
16	177.5	20.7	427	1	TR1A_BOVIN
17	169.5	19.8	417	1	TR16_HUMAN
18	168.5	19.6	425	1	TR16_MOUSE
19	167	19.5	283	1	Q820w1 mus musculu
20	164.5	19.2	326	1	TR16_RAT
21	164.5	19.2	386	1	TR14_HUMAN
22	164.5	19.2	417	1	VT2_MYXVL
23	164.5	19.2	655	1	Q9ubn6 homo sapien
24	163.5	19.1	416	1	TR12_HUMAN
25	163.5	19.1	655	1	Q9epu5 mus musculu
26	160	18.6	259	1	TR16_CHICK
27	156	18.2	325	1	TR21_HUMAN
28	156	18.2	468	1	TR10C_HUMAN
29	151	17.6	381	1	Q924m4 mus musculu
30	150.5	17.5	415	1	Q9qzm4 mus musculu
31	150	17.5	416	1	TNR3_MOUSE
32	148.5	17.3	300	1	Q9j1l3 mus musculu
33	148.5	17.3	461	1	TR6B_HUMAN
					P20333 homo sapien

34	148	17.2	250	1	TNR7_MOUSE
35	147.5	17.2	401	1	TNR7_MOUSE
36	146.5	17.1	401	1	TR1B_MOUSE
37	146	17.0	435	1	TR1B_RAT
38	144.5	16.8	474	1	TNR3_HUMAN
39	144	16.8	401	1	TNR3_HUMAN
40	143.5	16.7	260	1	TR1B_MOUSE
41	143	16.7	271	1	TR1B_HUMAN
42	143	16.7	498	1	TNR4_RAT
43	138	16.1	595	1	TNR8_MOUSE
44	136.5	15.9	1790	1	TNR8_HUMAN
45	135.5	15.8	493	1	LMB1_DROME
					TNR8_RAT

ALIGNMENTS

RESULT 1

TR23_MOUSE
ID TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63: Q8VHCO;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF1A1 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
implications for a novel imprinting centre and extended imprinting";
RL Hum. Mol. Genet. 9:2691-2706(2000).
[2]
SEQUENCE FROM N.A.
Pan G., Mao W., Risser P.;
"Characterization of SOB, a member of the TNFR family";
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
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EMBL; AJ278264; CAC16405.1; -
DR EMBL; AJ276505; CAC27352.1; -
DR EMBL; AY046550; AAL05072.1; -
DR HSSP; P19438; 1EXT.
DR MGD; MGI:1930269; Tnfrsf23.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9
FT SIGNAL-ANCHOR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT REPEAT 31 176
FT REPEAT 37 72
FT REPEAT 74 114
FT TNFR-CYS 1.
FT TNFR-CYS 2.

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FT REPEAT 115 155 TNFR-CYS 3.
FT DISULFID 38 49 BY SIMILARITY.
FT FT 50 63 BY SIMILARITY.
FT DISULFID 53 72 BY SIMILARITY.
FT DISULFID 75 90 BY SIMILARITY.
FT DISULFID 93 106 BY SIMILARITY.
FT DISULFID 96 114 BY SIMILARITY.
FT DISULFID 116 131 BY SIMILARITY.
FT DISULFID 134 147 BY SIMILARITY.
FT DISULFID 137 155 BY SIMILARITY.
FT CARBOHYD 148 148 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DDB7D CRC64;

Query Match 100.0%; Score 858; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.le-66;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMPESYFNCNPDGEYQSDNDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 29 AMPESYFNCNPDGEYQSDNDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 88
QY 61 DCELCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCPTCKPQGPVLPQECN 120
DB 89 DCELCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCPTCKPQGPVLPQECN 148
QY 121 STANTVCSYSSVSNPRNWLFLMLIVFCI 148
DB 149 STANTVCSYSSVSNPRNWLFLMLIVFCI 176

RESULT 2
TR22_MOUSE STANDARD; PRT; 180 AA.
AC Q9R62; O9CZ44; Q8VBH9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis
DE factor receptor p60 homolog 2) (TNF receptor family member SOBA).
GN TNFRSF22 OR TNFRSF12 OR TNFRH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Rissler P., Mao W., Baldwin D.T., Pan G.;
RA "Characterization of SOBA, a murine member of the TNFR family.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; AJ278265; CAC16406.1; -
CC EMBL; AJ276505; CAC27353.1; -
CC EMBL; AY048553; AAL05073.1; -
CC EMBL; AK012838; BAB28502.1; -
CC DR HSSP; PI9438; 1EXT.
CC DR MGD; MGI:1930270; Tnf1rsf22.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR Pfam; PF00020; TNFR_c6; 3.
CC DR SMART; SM00208; TNFR; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
CC DR PROSITE; PS00550; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT FT 42 180 EXTRACELLULAR (POTENTIAL).
FT REPEAT 47 82 TNFR-CYS 1.
FT REPEAT 84 124 TNFR-CYS 2.
FT REPEAT 125 165 TNFR-CYS 3.
FT DISULFID 48 59 BY SIMILARITY.
FT DISULFID 60 73 BY SIMILARITY.
FT DISULFID 63 82 BY SIMILARITY.
FT DISULFID 85 100 BY SIMILARITY.
FT DISULFID 103 116 BY SIMILARITY.
FT DISULFID 106 124 BY SIMILARITY.
FT DISULFID 126 141 BY SIMILARITY.
FT DISULFID 144 165 BY SIMILARITY.
FT DISULFID 147 165 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 12 12 L->V (IN REF. 3).
FT CONFLICT 171 180 RRSASVAVPI -> NPNRFLFLL (IN REF. 2).
SQ SEQUENCE 180 AA; 20226 MW; F8F5E165ADD53FA CRC64;

Query Match 74.7%; Score 641; DB 1; Length 180;
Best Local Similarity 84.8%; Pred. No. 3.5e-48;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 AMPESYFNCNPDGEYQSDNDVCKTCPSGTFVKAPCKIPHTQGCCKCHPGTFTGKDNGLH 60
DB 39 AMLEHSHFKCPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQGCCKCHPGTFTGKDNGLH 98
QY 61 DCELCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCPTCKPQGPVLPQECN 120
DB 99 ACTLCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCPTCKPQGPVLPQECN 158
QY 121 STANTVCSYSSVS 132
DB 159 STANTVCSYSSVS 170

RESULT 3
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FT CARBOHYD 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 332 AA; 37592 MW; 58903682756BF1B CRC64;

Query Match 26.4%; Score 226.5; DB 1; Length 332;
Best Local Similarity 29.9%; Pred. No. 1.2e-12;
Matches 43; Conservative 28; Mismatches 62; Indels 11; Gaps 5;

QY 10 CPDGEYSDNVCCKTFGTFVAPKCPKIPHTQGOCEKCHPG-TFTGKDNLGHLHDELCSTC 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 46 CPEQHREGQFCQCPGPGGRKRRADCTSPGAPQCVPCSEGEDYTDKNHHSKRCRCVC 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 DKQDNMVAD--CSATSDRKCEQIGLYYYDPKFPESRCPCPKQGPVPLQECNSTANTV 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 DGEHGLEVERKNCRTQNTQKCRKNPFCHTSQC-EHCNPCTTCEHG-VIENCTPTSTNK 162
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 C-----SSSVSNPNRWLFLEMLIV 145
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 CREVFQSGAGSRNLHWLWALLILI 186
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
DE (CD95).
DE DE
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RT Yoo J., Stone R.T., Beattie C.W.;
RA "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL; U34794; AAC48546.1; .
CC HSSP; P25445; 1DDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001388; TNFR_c6.
DR Pfam; PF000020; TNFR_c6; 3.
DR Pfam; PF000531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.

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DR HSP: P19438: 1EXT.
DR MGI:1314884; Tnftrsla.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR Pfam: PF00531; death; 1.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 454
FT DOMAIN 22 212
FT TRANSMEM 213 235
FT DOMAIN 236 454
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 339 349
FT DOMAIN 356 441
FT DISULFID 44 54
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 195
FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 202 202
FT CONFLICT 394 394
FT SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 25.1%; Score 215.5; DB 1; Length 454;
Best Local Similarity 28.1%; Pred. No. 1.4e-11;
Matches 52; Conservative 23; Mismatches 61; Indels 49; Gaps 7;

QY 10 CPDGEY---QSNVCKTCPSGTFVKAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCLECS 66
DB 44 CPOGKYVHSKNSICCTKCHKGTLYLVSDCPSGRDVTVCCEKGTFTASQNYLRQCLSK 103
QY 67 TCDKQNMV--ADCSATSDRKCEC---OIGLYYDYPKFPESCRCCTKCPQGIPLVQECNS 121
DB 104 TCRKMSQVEISPCQADKDTVCGCKNQFQYLSETHF--QCVDCCSPFNG-TWTIPCKE 160
QY 122 TANTVCS-----SSVSNNRN-----NLFLLML 143
DB 161 TQNTVCMCHAGFLRESECVPCSHCKKNECMKLCPLPPPLANVTNPQDSGTAFLVLPVL 220
QY 144 IVFCI 148
DB 221 LGCL 225

RESULT 6
ID CRMB_COWPX
AC 073559; STANDARD; PRT; 351 AA.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble TNF receptor II precursor (cytokine response modifying protein
DE B).
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GN (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRI-90 / Grishak;
RA MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins.";
RL Virology 243:432-460(1998).
RN [2]
RP FUNCTION.
RC STRAIN-Brighton red;
RX PubMed=8091685;
RA Hu F.O., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor.";
RL Virology 204:343-356(1994).
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC the modification of TNF-mediated antiviral processes.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL: Y11842; CAA72578.1; -.
DR EMBL: Y15035; CAA75306.1; -.
DR HSP; O14763; IDOG.
DR InterPro: IPR001368; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 351
FT REPEAT 31 67
FT REPEAT 69 110
FT DISULFID 32 43
FT DISULFID 44 57
FT DISULFID 47 67
FT DISULFID 70 85
FT DISULFID 88 102
FT DISULFID 92 110
FT CARBOHYD 103 103
FT CARBOHYD 191 191
FT CARBOHYD 250 250
FT SEQUENCE 351 AA; 38253 MW; 57CAE73EF4E5D7C7 CRC64;

Query Match 24.7%; Score 211.5; DB 1; Length 351;
Best Local Similarity 38.7%; Pred. No. 2.5e-11;
Matches 48; Conservative 14; Mismatches 55; Indels 7; Gaps 5;

QY 10 CPDGEYQSNVCKTCPSGTFVKAPC-KTPHTQGOCEKCHPGTFTGKDNGLHDCLECS-T 67
DB 32 KADNEYNHNLCLSCPPGTYASRLCDSYNTNTQCTPCSGTFTSRNHLFACLSNCR 91
QY 68 CDKQNMVADCSATSDRKCECQIGLYYDYPKFPESCRCPC---TKCPQGIPLVQECNSTAN 124
DB 92 CDSNQVETRSCNTHTNRICECAPG-YICLLKGSSGKACVCSQTKCGIGYGVSGH-TSTGD 149
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QY 125 TVCS 128
Db 150 VCS 153

RESULT 7

TRIA_RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91Y93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Wilder R.L., Remmers E.F.;
RA "Polymorphisms of the tumor necrosis factor receptor type 1 locus
among autoimmune susceptible and resistant inbred rat strains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (by similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC EMBL; M63122; AAA42256.1; -
CC EMBL; AF329976; AAK53562.1; -
CC EMBL; AF329977; AAK53563.1; -
CC EMBL; AF329981; AAK53567.1; -
CC EMBL; AF329978; AAK53564.1; -
CC EMBL; AF329979; AAK53565.1; -
CC EMBL; AF329980; AAK53566.1; -
CC PIR; B36555; B36555.
CC HSP; P19438; INCF.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00331; death; 1.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 1A.
FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 234 POTENTIAL.
FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 363 448 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 230 230 I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT VARIANT 295 295 DA/BKL AND F344/NHSD).
FT VARIANT 295 295 H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
Query Match 24.5%; Score 210; DB 1; Length 461;
Best Local Similarity 27.4%; Pred. No. 4.1e-11;
Matches 52; Conservative 22; Mismatches 62; Indels 54; Gaps 7;
QY 10 CPDGEY---QSDVCCCTCPSTGTFVAPCKIPHTGOCCKCHPGCTFTGKNGLHDCCLCS 66
Db 44 CPOGYAHPKNNISICCKHKGTYLVSDCPSGQETVCEVCDKGTFTTASQNHVRQCCLSK 103
QY 67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRCPTCKPQGIPIVQECNS 121
Db 104 TKRMEFQVEISPKADMDFVCGCKKNQFORLYSETHF--QCVDCCPCFNG--TVTTPCKE 160
QY 122 TANTVCS-----SSVSNPRN-----WL 138
Db 161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQCEMKLCLPPVANVTNPQDSGTAVLLPLVIEL 220
QY 139 FLMLIVFCI 148
Db 221 GLCLFFICI 230
RESULT 8
CRMB_CAMPS
ID CRMB_CAMPS STANDARD; PRT; 349 AA.
AC Q8UYA7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble TNF receptor II precursor (cytokine response modifying protein
DE B).
GN (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).

[7] SEQUENCE FROM N.A.
RC TISSUE-Muscle;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[8]
RN
RP SEQUENCE OF 41-45.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors";
RL J. Biol. Chem. 265:1531-1536(1990).
[9]
RN X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RT Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
beta complex: implications for TNF receptor activation";
RL Cell 73:431-445(1993).
[10]
RN X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE=97094982; PubMed=8939750;
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis
factor receptor";
RL Structure 4:1251-1262(1996).
[11]
RN VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX MEDLINE=99213501; PubMed=1019409;
RA McDermott M.F., Akentjevich I., Galon J., McDermott E.M.,
RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
RA Schlingens R., Kumarajewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
RA Hitman G.A., O'Shea J., Kastner D.L.;
RT "Germline mutations in the extracellular domains of the 55 kDa TNF
receptor, TNFR1, define a family of dominantly inherited
autoinflammatory syndromes";
RL Cell 97:133-144(1999).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
signaling complex (DISC) performs caspase-8 proteolytic activation
which initiates the subsequent cascade of caspases (aspartate-
specific cysteine proteases) mediating apoptosis. Contributes to
the induction of noncytotoxic TNF effects including anti-viral
state and activation of the acid sphingomyelinase.
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS SPECIFICALLY
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC -!- PTM: The soluble form is produced from the membrane form by
proteolytic processing.
CC -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
familial hibernian fever (FHF), a disease characterized by
recurrent fever, abdominal pain, localized tender skin lesions and
myalgia.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".

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DR EMBL; X55313; CAA39021.1; -
DR EMBL; M33294; AAA03210.1; -
DR EMBL; M58286; AAA36753.1; -
DR EMBL; M63121; AAA36754.1; -
DR EMBL; M75866; AAA61201.1; -
DR EMBL; M75864; AAA61201.1; JOINED.
DR EMBL; M75865; AAA61201.1; JOINED.
DR EMBL; M60275; AAA36756.1; -
DR EMBL; A21522; CAA01558.1; -
DR EMBL; BC010140; RAH10140.1; -
DR PIR; A34899; GQHUT1.
DR PIR; A35010; A35010.
DR PIR; S12057; S12057.
DR PIR; A38208; A38208.
DR PDB; 1TNR; 31-JUL-94.
DR PDB; 1NCF; 07-DEC-95.
DR PDB; 1EXT; 11-JAN-97.
DR Genew; HGNC:11916; TNFRSF1A.
DR MIM; 191190; -
DR MIM; 142680; -
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
DR PROSITE; PS00107; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW Disease mutation; Polymorphism; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR
FT CHAIN 41 291 SUPERFAMILY MEMBER 1A, MEMBRANE FORM.
FT DOMAIN 22 211 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT TRANSMEM 212 234 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 235 455 POTENTIAL.
FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).
FT REPEAT 83 125 TNFR-CYS 1.
FT REPEAT 126 166 TNFR-CYS 2.
FT REPEAT 167 196 TNFR-CYS 3.
FT REPEAT 338 348 TNFR-CYS 4.
FT DOMAIN 356 441 N-SMASE ACTIVATION DOMAIN (NSD).
FT DISULFID 44 58 DEATH.
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179

Query Match 23.4%; Score 200.5; DB 1; Length 455;
Best Local Similarity 33.6%; Pred. No. 2.6e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

QY 10 CPDGEY---QSNDDVCKTCPSGTFVKAPCKIPHTQCEKCHPCTFTGKDNGLHDCELCS 66
DB 44 CPQGRYIHFNPNNSICCTCKHKGYLYNDPCPGQDTCRCESGSGFTASENHLRLHCLSCS 103
QY 67 TCDKQDNW--ADCSATSDRKCECQIGLY-YDYPKFPESCRPCTKCPQGIPLVQECNSTA 123

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98273505; PubMed=9613449;
RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
RT (TNF)-receptor 1";
RL Vet. Immunol. Immunopathol. 61:379-385(1998).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (by similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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EMBL; U90937; AAB65143.1; -
DR HSP; P19438; 1TNR.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF000020; TNFR_c6; 3.
DR Pfam: PF00531; death; 1.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 471
FT
FT DOMAIN 22 210
FT TRANSMEM 211 233
FT DOMAIN 234 471
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 195
FT DOMAIN 340 360
FT DOMAIN 372 457
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81

FT	DISULFID	84	99	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	105	125	BY SIMILARITY.
FT	DISULFID	127	143	BY SIMILARITY.
FT	DISULFID	146	158	BY SIMILARITY.
FT	DISULFID	149	166	BY SIMILARITY.
FT	DISULFID	168	179	BY SIMILARITY.
FT	DISULFID	182	194	BY SIMILARITY.
FT	DISULFID	185	190	BY SIMILARITY.
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	471 AA;	51367 MW;	5243EF514DFE81C4 CRC64;

Query Match 21.7%; Score 186.5; DB 1; Length 471;
Best Local Similarity 32.6%; Pred. No. 4.2e-09;
Matches 42; Conservative 16; Mismatches 54; Indels 17; Gaps 6;

QY	10	CPDGEY---	QSDNVCKTCPSGTFVVRAPCKIPHTQGCCEKCHPGTFTGKONGHLHDLCS	66
DB	44	CPOGKYNHPQNSTICCTCKHGYLYVNDPCPGGRDTCRCVCAPTVTALENHLRRLCS	103	
QY	67	TCDDK--QNMVADCSATSDRKEC---	QIGLYYDVKFPESCRCTKCPQG---	118
DB	104	RCDEMFPQVEISPCVVDRDVTVCGRKNQYREYWGTF---	RCLNCSLCPNGTVNIP----	157
QY	119	CNSTANTVC	127	
DB	158	CQERQDTIC	166	

Search completed: December 10, 2002, 15:06:17
Job time : 9.30864 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:03:51 ; Search time 24.2099 Seconds
(without alignments)
1259.609 Million cell updates/sec

Title: US-09-855-266A-2

Perfect score: 858

Sequence: 1 AMPESYFNCPCGEYQSDV.....SSVSNPRNWLFLMLIVFCI 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288.5	33.6	438	13 Q9DFV0	Q9dfv0 brachydanio
2	246.5	28.7	357	13 Q9DF34	Q9df34 brachydanio
3	220.5	25.5	327	6 Q97491	Q97491 ovis aries
4	218.5	25.5	263	6 Q9XS60	Q9xs60 oryctolagus
5	218.5	25.5	320	6 Q9XS29	Q9xs29 oryctolagus
6	217.5	25.3	189	6 Q95185	Q95185 felis silve
7	217.5	25.3	319	6 Q9TV79	Q9tv79 oryctolagus
8	215.5	25.1	446	6 Q95ND3	Q95nd3 felis silve
9	214.5	25.0	347	12 Q97119	Q97119 cowpox viru
10	214.5	25.0	351	12 Q97121	Q97121 cowpox viru
11	211.5	24.7	348	12 Q97103	Q97103 monkeypox v
12	211.5	24.7	348	12 Q97108	Q97108 monkeypox v
13	211.5	24.7	348	12 Q97277	Q97277 monkeypox v
14	211.5	24.7	349	12 Q97101	Q97101 monkeypox v
15	211.5	24.7	349	12 Q97102	Q97102 monkeypox v
16	211.5	24.7	349	12 Q97291	Q97291 monkeypox v

17	211.5	24.7	351	12 Q73559	Q73559 cowpox viru
18	209.5	24.4	326	12 Q57120	Q57120 cowpox viru
19	209.5	24.4	360	12 Q57118	Q57118 cowpox viru
20	208.5	24.3	349	12 Q57098	Q57098 camelppox vi
21	208.5	24.3	349	12 Q57099	Q57099 monkeypox v
22	208.5	24.3	349	12 Q8UYA7	Q8uya7 camelppox v
23	208.5	24.3	349	12 Q57284	Q57284 camelppox vi
24	207.5	24.2	189	6 Q97530	Q97530 canis fami
25	207.5	24.2	326	12 Q57122	Q57122 cowpox viru
26	207.5	24.2	351	12 Q57117	Q57117 cowpox viru
27	205.5	24.0	349	12 Q57100	Q57100 monkeypox v
28	205.5	24.0	349	12 Q57109	Q57109 variola vir
29	204.5	23.8	347	12 Q57115	Q57115 cowpox viru
30	204.5	23.8	349	12 Q57305	Q57305 cowpox viru
31	202.5	23.6	349	12 Q57097	Q57097 camelppox vi
32	200.5	23.4	348	12 Q57112	Q57112 variola vir
33	200.5	23.4	348	12 Q85407	Q85407 variola vir
34	200.5	23.4	349	12 Q57110	Q57110 variola vir
35	200.5	23.4	349	12 Q57111	Q57111 variola vir
36	200.5	23.4	349	12 Q89098	Q89098 variola vir
37	200.5	23.4	349	12 Q89118	Q89118 variola vir
38	197.5	23.0	355	12 Q85308	Q85308 cowpox viru
39	195.5	22.8	350	12 Q57123	Q57123 cowpox viru
40	190.5	22.2	331	6 Q9T5N4	Q9tsn4 macaca fasc
41	190.5	22.2	331	6 Q9BDN0	Q9bdn0 macaca neme
42	190.5	22.2	350	12 Q57116	Q57116 cowpox viru
43	190	22.1	186	12 Q72735	Q72735 cowpox viru
44	190	22.1	186	12 Q91185	Q91185 vaccinia vi
45	189.5	22.1	331	6 Q9BDN4	Q9bdn4 cercocebus

ALIGNMENTS

RESULT 1

Q9DFV0	ID	Q9DFV0	PRELIMINARY:	PRT:	438 AA.
AC	Q9DFV0:				
DC	01-MAR-2001 (Tremblrel. 16, Created)				
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)				
DF	01-JUN-2002 (Tremblrel. 21, Last annotation update)				
DE	Ovarian TNF receptor.				
GN	TNFRSFA.				
OS	Brachydanio rerio (Zebrafish) (Zebra danio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
OX	NCBI_TaxID=7955;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RP	Boe J., Goetz F.W.;				
RT	"Molecular cloning and expression of a TNF receptor and two TNF				
RL	ligands in the fish ovary."				
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).				
DR	EMBL; AF250042; AAG24365.1;				
DR	HSSP; O14763; 1D0G				
DR	ZFIN; ZDB-GENE-010802-1; tnfrsfa.				
DR	InterPro; IPR000345; CytC_heme_bind.				
DR	InterPro; IPR000488; Death.				
DR	InterPro; IPR001368; TNFR_c6.				
DR	Pfam; PF00531; death; 1.				
DR	Pfam; PF00020; TNFR_c6; 3.				
DR	SMART; SM00005; TNFR; 1.				
DR	SMART; SM00208; TNFR; 3.				
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.				
DR	PROSITE; PS0017; DEATH_DOMAIN; 1.				
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.				
DR	PROSITE; PS00500; TNFR_NGFR_2; 2.				
KW	Receptor.				
SQ	SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;				
Query Match	33.6%;	Score	288.5;	DB	13;
Best Local Similarity	35.1%;	Pred. No.	1.5e-24;	Length	438;


```

Matches 53; Conservative 22; Mismatches 59; Indels 17; Gaps 2;

Qy 14 EYQNDVCKTCPSGTFVKAPCKIPHTGOQCEKCHPGTFTGKNGLDHCELCSTCDKQDN 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 EYPHNGFCKNCEAGTYVKEKCTSHVGMKSCPKCEKGTVAEHTGMEQCLQCSQCHRDQT 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 74 MVADCSATSDRKCEQIGLYYYDPKFPESCRCPTKCPGIPVLQECNSTANTVVC----- 127
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 109 VVAECTSTNTKCDCKFTGFLPDPEVCVKCKTKCKADEEVSCTPTSTNTKCRRRPSY 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 128 -----SSSVSNPRNWLFL-----LMLLVFC 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 PTEGTEKPSASNSTGTFIVIVSILIVIC 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
Q9DF34
ID Q9DF34 PRELIMINARY; PRT; 357 AA.
AC Q9DF34; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Death receptor.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
   receptor in transgenic zebrafish.";
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL; AF302789; AAC21396.1; -.
DR HSSP; P19438; IEXT.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;

Query Match 28.7%; Score 246.5; DB 13; Length 357;
Best Local Similarity 31.1%; Pred. No. 7.1e-20;
Matches 47; Conservative 30; Mismatches 67; Indels 7; Gaps 3;

Qy 5 SYSNCPDG-EYQNDVCKTCPSGTFVKAPCKIPHTGOQCEKCHPGTFTGKNGLDHCE 63
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 36 SRDVSRCRGLEYPHENICLNCPCAGTYVKKACAAAERGVCAPCEDFTVTEHDHGLKCI 95
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 64 LSCDCKDQNVADCSATSDRKCEQIGLYYYDPKFPESCRCPTKCPGIPVLQECNSTA 123
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 96 SCDCRIDQETIEKCTSTNTQTKCRNGSFLPDQACEVCKCRCKEDEFTEKSCTAIS 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 124 NTVV-----SSSVSNPRNWLFLMLLVF--CI 148
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 NTVCKRNSPGSSTSMTFIVIMPLIVLLACV 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
O97491
ID O97491 PRELIMINARY; PRT; 327 AA.
AC O97491;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fas protein.

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GN FAS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=LYMPHOCTE;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE397A CRC64;

Query Match 25.7%; Score 220.5; DB 6; Length 327;
Best Local Similarity 30.6%; Pred. No. 5.9e-17;
Matches 44; Conservative 28; Mismatches 65; Indels 7; Gaps 5;

Qy 9 NCPDGEYQNDVCKTCPSGTFVKAPCKIPHTGOQCEKCHPGT-FTGKNGLDHCELCST 67
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 46 SQOGLYREHLFCOPCPGKRRKNGDKRDGMPECLGSEGNEDTKSHSHDKIRCISV 105
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 68 CDKDONWVAD--CSATSDRKCEQIGLYYYDPKFPESCRCPTKCPGIPVLQECNSTANT 125
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 106 CDEEHGLEVEHNCTQNTQTKCRCKSN-FFCNSSPCHECNCTTCEHGI--IEKCTPTST 162
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 126 VCSSVSNNPRN-WLFLMLLVFCI 148
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 163 KCKGSRSHNTSLWALLILLILLILI 186
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RESULT 4
Q9XS60
ID Q9XS60 PRELIMINARY; PRT; 263 AA.
AC Q9XS60;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fas antigen spliced variant.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021297; BAA78429.1; -.
DR HSSP; O14763; 1D4V.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADED1BFD7 CRC64;

Query Match 25.5%; Score 218.5; DB 6; Length 263;
Best Local Similarity 33.1%; Pred. No. 7.9e-17;
Matches 46; Conservative 19; Mismatches 63; Indels 11; Gaps 5;

Qy 15 YQSDNVCKTCPSGTFVKAPCKIPHTGOQCEKCHPG-TFTGKNGLDHCELCSTCDKQDN 73

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Db 38 YLSGNFCCQLCPPTKKKADCTSNEGKPCQEGEYTDKSHFSSKRCRCLDGEHG 97
QY 74 M--VADCSATSDRKCEQIGLYYDFPESCRPCTKCPGIPVLQECNSTANTVCSVV 131
Db 98 LEVETDCTTQNTKCRCKSNFFCNALCK-EHCDPCTMCEHGI--IEECTQTSNTKCKEKG 154
QY 132 SNPRN-----WLFLLMLIV 145
Db 155 STTGSKHHFLWLLCILLI 173

RESULT 5
Q9XS29 ID Q9XS29 PRELIMINARY; PRT; 320 AA.
AC Q9XS29;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-type FAS antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021299; BAA78431.1; -.
DR EMBL; AB021296; BAA78428.1; -.
DR HSSP; P25445; 1DDF.
DR SMART; SM00208; TNFR_3.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
SQ SEQUENCE 320 AA; 36102 MW; DA235E243220FFB3 CRC64;

Query Match 25.5%; Score 218.5; DB 6; Length 320;
Best Local Similarity 33.1%; Pred. No. 9.7e-17;
Matches 46; Conservative 19; Mismatches 63; Indels 11; Gaps 5;

QY 15 YOSNDVCCCTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDCELCSTCDKQDN 73
Db 38 YLSGNFCCQLCPPTKKKADCTSNEGKPCQEGEYTDKSHFSSKRCRCLDGEHG 97
QY 74 M--VADCSATSDRKCEQIGLYYDFPESCRPCTKCPGIPVLQECNSTANTVCSVV 131
Db 98 LEVETDCTTQNTKCRCKSNFFCNALCK-EHCDPCTMCEHGI--IEECTQTSNTKCKEKG 154
QY 132 SNPRN-----WLFLLMLIV 145
Db 155 STTGSKHHFLWLLCILLI 173

RESULT 6
Q95185 ID Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
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RN [1]
RP SEQUENCE FROM N.A.
RA Duthie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA, partial cds.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS0050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 25.3%; Score 217.5; DB 6; Length 189;
Best Local Similarity 35.1%; Pred. No. 7.4e-17;
Matches 46; Conservative 16; Mismatches 62; Indels 7; Gaps 4;

QY 4 ESYFNCPDGEY---QSNADVCCCTCPSGTFVKAPCKIPHTQGOCEKCHPGTFTGKDNGLH 60
Db 38 EKRAIPCPQGYIHPQDNSICCTCKCHKGYLYNDCEGGLDTCRCENGTFITASENYLR 97
QY 61 DCELCSTCDK--QNMVADCSATSDRKCEQIGLY-YDFPKPESCRPCTKCPGIPVLQ 117
Db 98 QCLSCSKCKEMYQVEISPTVYRDTVCGRKNQRYWSETHFQCLNCSLCLNG-TVOI 156
QY 118 ECNSTANTVCS 128
Db 157 SCKETQNTVCT 167

RESULT 7
Q9TV79 ID Q9TV79 PRELIMINARY; PRT; 319 AA.
AC Q9TV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021298; BAA78430.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match 25.3%; Score 217.5; DB 6; Length 319;
Best Local Similarity 34.8%; Pred. No. 1.3e-16;
Matches 48; Conservative 16; Mismatches 63; Indels 11; Gaps 5;

QY 15 YOSNDVCCCTCPSGTFVKAPCKIPHTQGOCEKCHPG-TFTGKDNGLHDCELCSTCDKQDN 73
Db 38 YLSGNFCCQLCPPTKKKADCTSNEGKPCQEGEYTDKSHFSSKRCRCLDGEHG 97
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Db 32 CKNEYKHHLLCLSCPPGTYASRLCDSKTNTQCTSCGSGTFSRNNHLPACLSCNGR 91
QY 68 CDKQNMVADCSATSDRKCECQIGLYYDPKFPESCRCPC---TKCPOGIPVLQECNSTAN 124
Db 92 CDSNQVETRSCNTHNRICECSPG-YCYLLKGSSGCRACVQTKCGMGYGVSGH-TSTGD 149
QY 125 TVCS 128
Db 150 VICS 153

RESULT 11
O57103
ID O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP STRAIN=ZAIRE-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -.
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 24.7%; Score 211.5; DB 12; Length 348;
Best Local Similarity 39.0%; Pred. No. 6.6e-16;
Matches 48; Conservative 12; Mismatches 56; Indels 7; Gaps 5;

QY 10 CPDGEYQSNVCCCTCPGTFVKA PKIPHTGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
Db 32 CKNEYRSRNLCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90
QY 69 DKQNMVADCSATSDRKCECQIGLYYDPKFPESCRCPC---TKCPOGIPVLQECNSTANT 125
Db 91 DSNQVETRSCNTHNRICECSPG-YCYLLKGSSGCRCTCISKTKCGIGYGV-SGYTSTGDV 148
QY 126 VCS 128
Db 149 ICS 151

RESULT 12
O57108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -.
DR HSSP; O14763; 1DOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 24.7%; Score 211.5; DB 12; Length 348;
Best Local Similarity 39.0%; Pred. No. 6.6e-16;
Matches 48; Conservative 12; Mismatches 56; Indels 7; Gaps 5;

QY 10 CPDGEYQSNVCCCTCPGTFVKA PKIPHTGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
Db 32 CKNEYRSRNLCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90
QY 69 DKQNMVADCSATSDRKCECQIGLYYDPKFPESCRCPC---TKCPOGIPVLQECNSTANT 125
Db 91 DSNQVETRSCNTHNRICECSPG-YCYLLKGSSGCRCTCISKTKCGIGYGV-SGYTSTGDV 148
QY 126 VCS 128
Db 149 ICS 151

RESULT 13
O57277
ID O57277 PRELIMINARY; PRT; 348 AA.
AC O57277;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog (J2R) (J2L).
GN CRMB OR J2R OR J2L.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-96-I-16;
RX MEDLINE=21592287; PubMed=11734207;
RA Sheelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA Sandakhchiev L.S.;
RT "Human monkeypox and smallpox viruses: genomic comparison.";
RL FEBS Lett. 509:66-70(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-96-I-16;
RA Sheelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
RA Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88543; AAB94378.1; -.
DR EMBL; U87841; AAB94358.1; -.
DR EMBL; AF380138; AAL40648.1; -.
DR EMBL; AF380138; AAL40648.1; -.
DR HSSP; O14763; 1DOG.
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057102

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 14:56:26 ; Search time 34.7654 Seconds
(without alignments)
674.581 Million cell updates/sec

Title: US-09-855-266a-1
Perfect score: 1000
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250520 residues
Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000	100.0	176	19 AAW80254	Amino acid sequenc
2	350.5	35.0	380	22 ABB09344	Novel human diagno
3	280	28.0	204	23 ABB81467	Murine TACH protei
4	209	20.9	461	11 AAR07450	Rat Tumour Necrosi
5	206.5	20.6	355	16 AAR85073	Cowpox virus T2-eq
6	206.5	20.6	355	22 AAB50524	Human tumour necro
7	206.5	20.6	455	11 AAR07451	Human Tumour Necro
8	205.5	20.5	168	13 AAR24084	Truncated TNF-alph
9	205.5	20.5	199	13 AAR24080	Truncated TNF-alph
10	205.5	20.5	211	20 AAW89225	Tumour necrosis fa

11	205.5	20.5	280	22 AAB66979	Tnfr1 protein. Un
12	205.5	20.5	311	20 AAW89229	Tumour necrosis fa
13	205.5	20.5	366	20 AAW89228	Tumour necrosis fa
14	205.5	20.5	371	11 AAR07449	Tumour Necrosis Fa
15	205.5	20.5	397	20 AAW89227	Tumour necrosis fa
16	205.5	20.5	417	20 AAW89226	Tumour necrosis fa
17	205.5	20.5	420	20 AAW89224	Tumour necrosis fa
18	205.5	20.5	455	12 AAR10986	30kD TNF inhibitor
19	205.5	20.5	455	12 AAR11082	Human 55kD TNF-bin
20	205.5	20.5	455	13 AAR24000	TNF-alpha 55kD rec
21	205.5	20.5	455	14 AAR42059	Lambda derived TNF
22	205.5	20.5	455	16 AAR5084	p55 TNF-R. Homo s
23	205.5	20.5	455	20 AAY30934	Human tumour necro
24	205.5	20.5	455	21 AAB36266	Human tumour necro
25	205.5	20.5	455	21 AAB37800	Human tumour necro
26	205.5	20.5	455	21 AAB26984	Human TNFR 1. Hom
27	205.5	20.5	455	21 AAB23446	Human tumour necro
28	205.5	20.5	455	21 AAB01336	TNF-R1 death recep
29	205.5	20.5	455	22 AAB66817	Human TNFBP-associ
30	205.5	20.5	455	22 AAB36697	Human tumour necro
31	205.5	20.5	455	22 AAB37677	Human 30 kDa TNF i
32	205.5	20.5	455	23 ABB81649	Human tumour necro
33	205.5	20.5	455	23 AAU75064	Human tumour necro
34	205	20.5	327	14 AAR41688	Murine Fas antigen
35	205	20.5	327	16 AAR78611	Murine Fas antigen
36	205	20.5	327	17 AAR92530	mFas sequenc. Sy
37	205	20.5	327	20 AAW86241	Fas ligand (FasL)
38	205	20.5	327	21 AAB19344	Amino acid sequenc
39	204.5	20.4	285	18 AAW33359	TBP(20-190)/hCG-al
40	204.5	20.4	455	13 AAR20787	TNF-alpha binding
41	204.5	20.4	658	23 AAM49759	TNF-selectokine pr
42	203	20.3	350	23 ABB81468	Viral CrmB protein
43	202.5	20.2	349	22 AAB50523	Human tumour necro
44	200.5	20.1	139	22 AAB66977	Peptide: SEQ ID 12
45	200.5	20.1	154	21 AAY94711	Tumour necrosis fa

ALIGNMENTS

RESULT 1

AAW80254

ID AAW80254 standard; Protein; 176 AA.

XX

AC AAW80254;

XX

DT 28-JAN-1999 (first entry)

XX

DE Amino acid sequence of protein 7F4.

XX

KW Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.

KW

XX

OS Unidentified.

XX

XX

Key Location/Qualifiers

FT Peptide 1..28

FT /note= "signal peptide"

FT Protein 29..176

FT /note= "mature protein"

XX

PN WO9843998-A1.

XX

PD 08-OCT-1998.

XX

PF 01-APR-1998; 98WO-JP01511.

XX

PR 01-APR-1997; 97JP-0099653.

XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Kimura N, Toyoshima T;

XX

DR WPI; 1998-568275/48.
 DR N-PSDB; AAV68046.
 XX
 PT Receptor protein inducing differentiation in osteoblast cells - has
 PT extracellular region only and can be used for screening substances
 PT for treatment of bone growth disorders
 XX
 PS Claim 1; Pages 29-31; 5lpp; Japanese.
 XX
 CC The present sequence represents a protein designated 7F4. This protein
 CC is capable of inducing differentiation in osteoblast cells. The
 CC protein may be used to screen compounds for the ability to bind to
 CC it, for use as ligands, agonists or antagonists and inhibiting or
 CC otherwise altering its differentiation inducing activity. Compounds
 CC so identified, as well as the protein itself, DNA encoding it, and
 CC antibodies to it, may be used in the treatment of diseases of bone
 CC growth and osteoblast differentiation, such as bone sarcomas.
 XX
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 1000; DB 19; Length 176;
 Best Local Similarity 100.0%; Pred. No. 1.5e-76;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVTFSHVSSLHWFLLLLNLFPLVIFAMPESYFNCPCDGEYQSDVCCKTCPSGTFVK 60
 Db 1 MVTFSHVSSLHWFLLLLNLFPLVIFAMPESYFNCPCDGEYQSDVCCKTCPSGTFVK 60
 QY 61 APCKIPHTQGOCEKCHPCTFTGKNGLDHCELCSTCDKDONMVDGCSATSDRKECQIGL 120
 Db 61 APCKIPHTQGOCEKCHPCTFTGKNGLDHCELCSTCDKDONMVDGCSATSDRKECQIGL 120
 QY 121 YYDPKFPESCRCPCPKCQIPVQLQECNSTANTVCSSVSNNRNWLFLLMLIVFCI 176
 Db 121 YYDPKFPESCRCPCPKCQIPVQLQECNSTANTVCSSVSNNRNWLFLLMLIVFCI 176
 RESULT 2
 ABG09344
 ID ABG09344 standard; Protein; 380 AA.
 XX
 AC ABG09344;
 XX
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #9335.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS73531.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX

PS Claim 20; SEQ ID No 39703; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 380 AA;
 Query Match 35.0%; Score 350.5; DB 22; Length 380;
 Best Local Similarity 57.6%; Pred. No. 1.3e-21;
 Matches 72; Conservative 3; Mismatches 17; Indels 33; Gaps 2;
 QY 7 VSSLSHWF-----LLLLLLNLFPLQKAVHRKATPESATADCSGRDCAPWKFAMLEL 107
 Db 48 VSSLSRWFRLRLRLRLRLRLRLPLQKAVHRKATPESATADCSGRDCAPWKFAMLEL 107
 QY 34 YSNCPDGEYQSDVCCKTCPSGTFVKAPCKIPHTQGOCEKCHPCTFTGKNGLDHCELC 93
 Db 108 HSFKCPAGEYWSKDVCCKNCAGTFVKAPCEIPHTQGOCEKCHPCTFTGKNGLDHCELC 167
 QY 94 STCDK 98
 Db 168 STCDK 172
 RESULT 3
 AB81467
 ID AB81467 standard; Protein; 204 AA.
 XX
 AC AB81467;
 XX
 DT 29-AUG-2002 (first entry)
 DE Murine TACH protein SEQ ID NO:2.
 XX
 KW TACH; tumour necrosis factor receptor family; TNF receptor; cancer;
 KW inflammatory; immunoregulatory; cytostatic; antiinflammatory;
 KW gene therapy.
 XX
 OS Mus sp.
 XX
 PN WO200228900-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US30993.
 PR 04-OCT-2000; 2000US-237791P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOX-) APOXIS BIOSCIENCES LTD.
 XX
 PI Zheng T, Tschopp J, Schneider P;
 XX WPI; 2002-507878/54.
 DR

The present invention describes the human TR1D protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive, neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TR1D polynucleotides are useful for detecting complementary polynucleotides. TR1D proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease.

Query Match	20.5%	Score 205.5;	DB 13;	Length 199;
Best local similarity	31.3%;	Pred. No. 1e-09;		
Matches	52;	Conservative	22;	Mismatches 75; Indels 17; Gaps 6;

QY	7	VSSLSHWFLLLLLNLFL----	PVIFAMP-----	ESYSFNCPDGEY---	OSNDVCCKTC	53	
		: ::	: ::	: ::	: ::	: ::	
Db	3	LSITVPDLLLPVLELLVGI	PSGVIGLPHLGDREKRD	SVCPGKVIHPONNSIC	TKC	62	
		: ::	: ::	: ::	: ::	: ::	
QY	54	PSGTFVAKPKIPHTQGC	CKHGTFTGKDNGLHDC	ELASTCDKDONMV--	ADCSATSD	111	
		: ::	: ::	: ::	: ::	: ::	
Db	63	HKGTYLNDYCPGQD	TDCRECSG	FTASENHLRHCLSC	SKRKEMQGV	ISSCTVDRD	122
		: ::	: ::	: ::	: ::	: ::	
QY	112	RKECQIGLY-YD	KPFKPSCRPCTK	PGQIPVLQEN	STANTVCS	156	
		: ::	: ::	: ::	: ::	: ::	
Db	123	TVCGCRKQRYH	WSENLFCQFNC	SLCLNG-TVHL	SQCEKONTVCT	167	
		: ::	: ::	: ::	: ::	: ::	

RESULT 10	
AAW89225	
ID	AAW89225 standard; Protein; 211 AA.
XX	
AC	AAW89225;
XX	
DT	04-MAR-1999 (first entry)
XX	
DE	Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.
XX	
KW	Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW	OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW	inflammation; apoptosis.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO9849305-A1.
XX	
PD	05-NOV-1998.
XX	
PF	29-APR-1998; 98WO-US08631.
XX	
PR	01-MAY-1997; 97US-0850188.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Boyle WJ, Wooden S;
XX	
DR	WPI; 1999-034661/03.
XX	
PT	New chimeric osteoprotegerin polypeptides - contain the
PT	osteoprotegerin dimerisation domain and a heterologous sequence,
PT	useful to treat TNF and TNFR-mediated disorders
XX	
PS	Example 1; Fig 4; 92pp; English.
XX	
CC	The present invention describes a chimeric polypeptide (A1), comprising
CC	an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC	amino acid sequence. Also described are: (1) a multimer polypeptide
CC	comprising covalently associated A1 monomers; (2) an isolated nucleic
CC	acid encoding A1; (3) an expression vector comprising the nucleic acid
CC	sequence; and (4) a host cell transformed or transfected with the
CC	expression vector so that the nucleic acid is expressible. The products
CC	from the present invention are useful to treat a variety of disorders
CC	including those related to receptor binding. Compositions comprising
CC	tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC	are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC	autoimmune diseases and disorders related to excessive apoptosis. The
CC	chimeras are also useful for detecting molecules which interact with
CC	fused heterologous sequences to identify potential new receptors and
CC	ligands. The present sequence represents a TNFbp/OPG construct from
CC	the example of the present invention for creating TNFbp/OPG fusion
CC	proteins.
XX	

CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock. The present sequence was used in a sequence
 CC homology comparison.

autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimera are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

QY	7	VSSLUSHFWLLLLLNLFL-----PVIFAMP-----ESYFNCDPGEY----	OSNDVCCKTC	53
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	3	LSTVPDLLLLPLVLELLANGIYPSGVIGIYVPHLGRKRDSCVPGKGIHPQNNISCTC	KTC	62
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	54	PSGFVFAKPKIPHTQGOCEKCHPGTFTFGKNGLHDCELCSTCDKDNWV--ADC	SATSD	111
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	63	HKGTYLNDPCPGQDPTDCRCESGFTASENHLRHCLSCSKCKEMQGVLEISCTVD	RD	122
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	112	RKCEQIGLY--YYDPKFPESCRCPTCKPQGIPTVLOECNSTANTVCS		156
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	123	TVCSGRNQRYHWSENLFCQFNCSLCLNG--TVHLSCOEKONTVCT		167
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:

RESULT 14	
AAAR07449	
ID	AAAR07449 standard; protein; 371 AA.
XX	
XX	
AC	AAAR07449;
XX	
DT	29-JAN-1991 (first entry)
XX	
XX	Tumour Necrosis Factor-Binding Protein from pTNF-Bp15 cDNA.
DE	
XX	
KW	Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW	pTNF-Bp15; infectious disease; parasitic disease; cachexia;
KW	autoimmune disease; shock.

XX	Sequence	371 AA;	
Qy	Query Match	20.5%; Score 205.5; DB 11; Length 371;	
B	Best Local Similarity	31.3%; Pred. No. 1.9e-09;	
M	Matches 52; Conservative	22; Mismatches 75; Indels 17; Gaps	
Qy	7	VSSLHWFLLLLINLFL-----PVIFAMP-----ESYFNCPPDGEY---QSNDCCKTC 53	
Db	3	LSTVPDLLPLVLELLLVGTPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISCTTK 62	
Qy	54	PSGTFVAPCKIPHTGQCEKCHPGFTGKDNGLHDCELCSTCDKQNMV--ADCSATSD 111	
Db	63	HKGTYLYNDPCPGQQDTCRECESGSFTASENHLRCLSCSKCKREMGOVEISSCTVDRD 122	
Qy	112	RKCEQIGLY-YDPRFPESCRCCTKCPGIPVLQECNSTANTVCS 156	
Db	123	TVCGCRKQRYHWSENLFOCFNCSICLNG-TVHLSCQEKQNTVCT 167	
RESULT	15		
AAW89227			
ID	AAW89227	standard; Protein; 397 AA.	
XX	AAW89227;		
XX	04-MAR-1999	(first entry)	
XX	Tumour necrosis factor bp/osteoprotegerin construct TNFBp/217.		
XX	Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;		
KW	OPG; chimeric; fusion; dimerisation domain; autoimmune disease;		
KW	inflammation; apoptosis.		
XX	Homo sapiens.		
OS	Synthetic.		
PN	W09849305-A1.		
XX	05-NOV-1998.		
XX	29-APR-1998;	98WO-0508631.	
XX	01-MAY-1997;	97US-0850188.	
XX	(AMGE-) AMGEN INC.		
XX	Boyle WJ, Wooden S;		
XX	WPI; 1999-034661/03.		
XX	New chimeric osteoprotegerin polypeptides - contain the		
PT	osteoprotegerin dimerisation domain and a heterologous sequence,		
PT	useful to treat TNF and TNFR-mediated disorders		
XX	Example 1; Fig 4; 92pp; English.		
XX	The present invention describes a chimeric polypeptide (A1), comprising		
CC	an osteoprotegerin (OPG) dimerisation domain fused to a heterologous		
CC	amino acid sequence. Also described are: (1) a multimer polypeptide		
CC	comprising covalently associated A1 monomers; (2) an isolated nucleic		
CC	acid encoding A1; (3) an expression vector comprising the nucleic acid		
CC	sequence; and (4) a host cell transformed or transfected with the		
CC	expression vector so that the nucleic acid is expressible. The product		
CC	from the present invention are useful to treat a variety of disorders		
CC	including those related to receptor binding. Compositions comprising		
CC	tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras		
CC	are used to treat TNF and TNFR-mediated disorders such as inflammation		
CC	autoimmune diseases and disorders related to excessive apoptosis. The		
CC	chimeras are also useful for detecting molecules which interact with		
CC	fused heterologous sequences to identify potential new receptors and		
CC	ligands. The present sequence represents a TNFBp/OPG construct from		
CC	the example of the present invention for creating TNFBp/OPG fusion		

CC proteins.

XX
SQ Sequence 397 AA;

Query Match 20.5%; Score 205.5; DB 20; Length 397;
Best Local Similarity 31.3%; Pred. No. 2.1e-09;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY	7	VSSLSHWFLILLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNQVCCCKTC	53
DB	3	LSTVPDLLPLVLLELLVGIYPSGIVGLVPHLGDREKRDVCPQCKYIHPQNNISICCTKC	62
QY	54	PSGTFVAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCSTCDKQNMV--ADCSATSD	111
DB	63	HKGTLYNDPCPGQDTCRECESGSFTASENHLRHCLSCSKRKEMQGVETISCTVDRD	122
QY	112	RKCEQIGLY--YYPDKFPESCRPCTKCPQGIPIVLOECNSTANTVCS	156
DB	123	TVCGCRKNQRYHWSENLFQCFNCSCLNG--TVHLSCQEKQNTVCT	167

Search completed: December 10, 2002, 15:05:52
Job time : 36.7654 secs

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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:46 ; Search time 12.4938 Seconds
(without alignments)
414.479 Million cell updates/sec

Title: US-09-855-266A-1

Perfect score: 1000

Sequence: 1 MVTFSHVSSLHWFLLLLL.....SSVSNPRNWLFLMLIVFCI 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000	100.0	176	4	US-09-411-722-1
2	858	85.8	148	4	US-09-411-722-2
3	206.5	20.6	355	1	US-08-292-549-6
4	206.5	20.6	355	4	US-09-006-353A-14
5	206.5	20.6	355	4	US-09-573-986-14
6	205.5	20.5	167	1	US-08-050-319B-2
7	205.5	20.5	167	1	US-08-050-319B-57
8	205.5	20.5	167	2	US-08-465-982-2
9	205.5	20.5	167	2	US-08-465-982-57
10	205.5	20.5	197	4	US-08-828-683A-21
11	205.5	20.5	280	3	US-08-974-022-46
12	205.5	20.5	280	4	US-08-795-445A-46
13	205.5	20.5	280	4	US-08-795-447A-46
14	205.5	20.5	280	4	US-08-974-186-46
15	205.5	20.5	280	4	US-08-795-446B-46
16	205.5	20.5	280	4	US-08-706-945D-132
17	205.5	20.5	455	1	US-08-050-319B-25
18	205.5	20.5	455	1	US-08-321-668-2
19	205.5	20.5	455	1	US-08-837-941-2
20	205.5	20.5	455	2	US-08-126-016-2
21	205.5	20.5	455	2	US-08-465-982-25
22	205.5	20.5	455	4	US-08-815-469-5
23	205.5	20.5	455	4	US-09-006-353A-3
24	205.5	20.5	455	4	US-09-527-236A-5
25	205.5	20.5	455	4	US-08-054-970-2
26	205.5	20.5	455	4	US-09-565-918-4
27	205.5	20.5	455	4	US-09-573-986-3

28	205	20.5	327	4	US-09-290-640-66	Sequence 66, Appl
29	204.5	20.4	199	1	US-08-050-319B-48	Sequence 48, Appl
30	204.5	20.4	199	2	US-08-465-982-48	Sequence 48, Appl
31	204.5	20.4	285	4	US-08-804-166-6	Sequence 6, Appl
32	204.5	20.4	285	4	US-08-910-991-6	Sequence 6, Appl
33	202.5	20.2	349	4	US-09-006-353A-13	Sequence 13, Appl
34	202.5	20.2	349	4	US-09-573-986-13	Sequence 13, Appl
35	200.5	20.1	139	4	US-08-706-945D-129	Sequence 129, App
36	200.5	20.1	153	2	US-08-219-237B-4	Sequence 4, Appl
37	200.5	20.1	153	4	US-08-477-347-12	Sequence 12, Appl
38	200.5	20.1	153	4	US-08-476-862-3	Sequence 3, Appl
39	200.5	20.1	153	4	US-08-468-560C-4	Sequence 4, Appl
40	200.5	20.1	154	4	US-08-828-683A-12	Sequence 12, Appl
41	200.5	20.1	161	4	US-09-326-394-2	Sequence 2, Appl
42	200.5	20.1	256	4	US-08-804-166-2	Sequence 2, Appl
43	200.5	20.1	256	4	US-08-910-991-2	Sequence 2, Appl
44	200.5	20.1	307	4	US-08-804-166-4	Sequence 4, Appl
45	200.5	20.1	307	4	US-08-910-991-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-411-722-1

; Sequence 1, Application US/09411722

; Patent No. 6271366

; GENERAL INFORMATION:

; APPLICANT: Kimura, Naoki

; APPLICANT: Toyoshima, Tomoko

; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

; FILE REFERENCE: 06501/040001

; CURRENT APPLICATION NUMBER: US/09/411,722

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: PCT/JP98/01511

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: JP 9/099653

; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 176

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-411-722-1

Query Match 100.0%; Score 1000; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVTFSHVSSLHWFLLLLLNLFLPVI FAMPESYSPNC PDGEYQSN DVCC KTCPSGTFVK 60

|||||

Db 1 MVTFSHVSSLHWFLLLLLNLFLPVI FAMPESYSPNC PDGEYQSN DVCC KTCPSGTFVK 60

|||||

OY 61 APCKIPHTGOCEKCHPGFTGKDNGLHDCELCSTCKDONMVADCSATSDRKECOIGL 120

|||||

Db 61 APCKIPHTGOCEKCHPGFTGKDNGLHDCELCSTCKDONMVADCSATSDRKECOIGL 120

|||||

OY 121 YYDPKFPESCRCPTKCPGIPVLQBCNSTANTVCSSVSNPRNWLFLMLIVFCI 176

|||||

Db 121 YYDPKFPESCRCPTKCPGIPVLQBCNSTANTVCSSVSNPRNWLFLMLIVFCI 176

|||||

RESULT 2

US-09-411-722-2

; Sequence 2, Application US/09411722

; Patent No. 6271366

; GENERAL INFORMATION:

; APPLICANT: Kimura, Naoki

; APPLICANT: Toyoshima, Tomoko

; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

; FILE REFERENCE: 06501/040001

; CURRENT APPLICATION NUMBER: US/09/411,722

;; CURRENT FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: PCT/JP98/01511
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: JP 9/099653
;; PRIOR FILING DATE: 1997-04-01
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 148
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-411-722-2

Query Match 85.8%; Score 858; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.3e-72;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AMPESYSFNCPCDGEYQSDVCCVCKTSPGTFVVKAPCKIPHTQCEKCHPGTFTGKDNGLH 88
Db 1 AMPEYSFNCPCDGEYQSDVCCVCKTSPGTFVVKAPCKIPHTQCEKCHPGTFTGKDNGLH 60
QY 89 DCELCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCCTKCPQGIPLVQECN 148
Db 61 DCELCSTCDKQNMVADCSATSDRCEQIGLYYYDPKFPESCRCCTKCPQGIPLVQECN 120
QY 149 STANTVCSVSNPRNWLFLMLIVFCI 176
Db 121 STANTVCSVSNPRNWLFLMLIVFCI 148

RESULT 3
US-08-292-549-6

;; Sequence 6, Application US/08292549
;; Patent No. 5464938

;; GENERAL INFORMATION:

;; APPLICANT: Smith, Craig A.
;; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Immunex Corporation
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98101

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/292,549

;; FILING DATE:

;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/963,330

;; FILING DATE: 10/19/92

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Perkins, Patricia A.

;; REGISTRATION NUMBER: 34,693

;; REFERENCE/DOCKET NUMBER: 2602-A

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (206) 587-0430

;; TELEFAX: (206) 233-0644

;; INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 355 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

US-08-292-549-6

Query Match 20.6%; Score 206.5; DB 1; Length 355;
Best Local Similarity 31.1%; Pred. No. 1.1e-11;
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;
QY 14 FLLLLLLNLFLPV--IFAMPESYSFNCPCDGEYQSDVCCVCKTSPGTFVVKAPC-KIPHTQG 70
Db 4 YILLLLLSCTIIINSIDITPHEPSNGKCKDNEYKRHHLLCCLSCPPGYVASRLCDSKKTNT 63
QY 71 QCEKCHPGTFTGKDNGLHDCELCS--TCDKQNMVADCSATSDRCEQIGLYYYDPKFP 129
Db 64 QCTPCASDTFTSRNHLPACLSCNGRCDNSQVETRSCTNTHNRICDCAPG--YFCFLKGS 122
QY 130 SCRPC---TKC-----POGIPVQEC-----NSTANTV--CSSSVSNPRNWL 166
Db 123 GCKACVQTKCGIGYGVSGHTPTGDDVVVCSGPCGLGTSHTVSSVDKCEPVPSTNFNYI 179

RESULT 4

US-09-006-353A-14
;; Sequence 14, Application US/09006353A
;; Patent No. 6261801

;; GENERAL INFORMATION:

;; APPLICANT: WEI, XING-FEI

;; APPLICANT: YU, GUO-LIANG

;; APPLICANT: GENTZ, REINER

;; APPLICANT: RUBEN, STEVEN

;; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

;; NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

;; STREET: 9410 KEY WEST AVENUE

;; CITY: ROCKVILLE

;; STATE: MD

;; COUNTRY: US

;; ZIP: 20850

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/006,353A

;; FILING DATE:

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: BROOKES, ANDERS A

;; REGISTRATION NUMBER: 36,373

;; REFERENCE/DOCKET NUMBER: PF341

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (301) 309-8504

;; TELEFAX: (301) 309-8512

;; INFORMATION FOR SEQ ID NO: 14:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 355 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

US-09-006-353A-14

Query Match 20.6%; Score 206.5; DB 4; Length 355;
Best Local Similarity 31.1%; Pred. No. 1.1e-11;
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;

QY 14 FLLLLLLNLFLPV--IFAMPESYSFNCPCDGEYQSDVCCVCKTSPGTFVVKAPC-KIPHTQG 70
Db 4 YILLLLLSCTIIINSIDITPHEPSNGKCKDNEYKRHHLLCCLSCPPGYVASRLCDSKKTNT 63
QY 71 QCEKCHPGTFTGKDNGLHDCELCS--TCDKQNMVADCSATSDRCEQIGLYYYDPKFP 129
Db 64 QCTPCASDTFTSRNHLPACLSCNGRCDNSQVETRSCTNTHNRICDCAPG--YFCFLKGS 122
QY 130 SCRPC---TKC-----POGIPVQEC-----NSTANTV--CSSSVSNPRNWL 166

[illegible]

```

; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-2

Query Match 20.5%; Score 205.5; DB 1; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPPDGEY---QSDNVCCCKTC 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 LSTVPDLLPLVLELLVGIYPSGVLGPHLGDRKRDVSCPGKVIHPQNNISICCTKC 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 54 PSGFTVAPKIPHTGQCKRCHPTGTTGKNDGLHDCELSTCDKQDNV--ADCSATSD 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 HKGTLYNDPCPGQDTRCECSGPTASENHLRLCLSCSKCKEMGQVEISSCTVDRD 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 112 RKCEQIGLY-YDPKPEPESCRPTCKPQGIPIVLOECNSTANTVCS 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 TVCGCRKNQRYHWSENLFCFCNCSLCLNG--TVHLSQCEKQNTVCT 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-08-050-319B-57
; Sequence 57, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P. W. Gray,
; APPLICANT: M. J. C. Turner, F. M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-57

Query Match 20.5%; Score 205.5; DB 1; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

OV 7 VSSLHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPPDGEY---QSDNVCCCKTC 53

```

```

; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-2

Query Match 20.5%; Score 205.5; DB 1; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPPDGEY---QSDNVCCCKTC 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 LSTVPDLLPLVLELLVGIYPSGVLGPHLGDRKRDVSCPGKYIHPQNNISICCTKC 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 54 PSGFVTRAPCKIPHTGQCKRCHPTGTTGKNDGLHDCELSTCDKQDNV--ADCSATSD 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 HKGTLYNDPCPGQDTRCECSGPTASENHLRLCLSCSKCKEMGQVEISSCTVDRD 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 112 RKCEQIGLY-YDPKPEPESCRPTCKPQGIPIVLOECNSTATVCS 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 TVCGCRKNQRYHWSENLFCFCNCSLCLNG--TVHLSQCKQNTVCT 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-08-050-319B-57
; Sequence 57, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P. W. Gray,
; APPLICANT: M. J. C. Turner, F. M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; NERVE OF INVENTION: Necrosis factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-57

Query Match 20.5%; Score 205.5; DB 1; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

OV 7 VSSLHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPPDGEY---QSDNVCCCKTC 53

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Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICCTKC 62
Qy 54 PSGETVAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCLELSTCDKDNQMV--ADCSATSD 111
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 122
Qy 112 RKCECQIGLY-YDYPKFPESCRCPTCKPQGIPLVLECNSTANTVCS 156
Db 123 TVCGCRKNQRYHWSLENLFCQFNCSLCLNG-TVHLSCQEKQNTVCT 167

RESULT 8
US-08-465-982-2
; Sequence 2, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-982-2

Query Match 20.5%; Score 205.5; DB 2; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

Qy 7 VSSLSHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNQVCCCTC 53
Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICCTKC 62
Qy 54 PSGETVAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCLELSTCDKDNQMV--ADCSATSD 111
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 122
Qy 112 RKCECQIGLY-YDYPKFPESCRCPTCKPQGIPLVLECNSTANTVCS 156
Db 123 TVCGCRKNQRYHWSLENLFCQFNCSLCLNG-TVHLSCQEKQNTVCT 167

RESULT 9
US-08-465-982-57
; Sequence 57, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-982-57

Query Match 20.5%; Score 205.5; DB 2; Length 167;
Best Local Similarity 31.3%; Pred. No. 6e-12;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

Qy 7 VSSLSHWFLLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNQVCCCTC 53
Db 3 LSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICCTKC 62
Qy 54 PSGETVAPCKIPHTQGOCEKCHPGTFTGKDNGLHDCLELSTCDKDNQMV--ADCSATSD 111
Db 63 HKGTLYNDPCPGQDTCRECESSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 122
Qy 112 RKCECQIGLY-YDYPKFPESCRCPTCKPQGIPLVLECNSTANTVCS 156
Db 123 TVCGCRKNQRYHWSLENLFCQFNCSLCLNG-TVHLSCQEKQNTVCT 167

RESULT 10
US-08-828-683A-21
; Sequence 21, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
```


RESULT 15
US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Lacey, David L.
; APPLICANT: Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:21 ; Search time 15.7531 Seconds
(without alignments)
1074.054 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MTFSSHVSSLHWHLLLLL.....SSVSNPRNWLFLMLIVFCI 176
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215.5	21.6	454	1 GQMT1	tumor necrosis fac
2	210.0	21.0	461	1 GQRT1	tumor necrosis fac
3	205.5	20.5	455	1 GQHT1	tumor necrosis fac
4	205.0	20.5	327	2 A46484	apoptosis-mediatin
5	204.0	20.4	348	2 T28623	hypothetical prote
6	202.5	20.2	349	2 D72175	G2R protein - vari
7	202.5	20.2	349	2 D36858	gene G4R protein -
8	194.0	19.4	324	2 JC2395	Fas antigen precu
9	193.5	19.4	461	2 JC4302	tumor necrosis fac
10	189.5	18.9	335	2 A40036	apoptosis-mediatin
11	184.0	18.4	651	2 JC7705	death receptor-6 -
12	183.0	18.3	427	1 GQHUN	nerve growth facto
13	177.0	17.7	314	2 I37383	FAS soluble protei
14	171.0	17.1	425	1 A26431	nerve growth facto
15	167.5	16.8	326	1 GOV2ML	T2 protein - myxom
16	166.5	16.7	416	1 JN0006	nerve growth facto
17	164.0	16.4	325	2 B43692	T2 protein - rabbi
18	152.0	15.2	461	1 A35356	tumor necrosis fac
19	150.0	15.0	271	2 I2783	OX40 antigen precu
20	150.0	15.0	435	2 I54182	tumor necrosis fac
21	149.0	14.9	595	2 A42086	CD30 antigen precu
22	148.0	14.8	250	1 A49053	CD27 antigen precu
23	145.0	14.5	260	1 A46517	CD27 antigen precu
24	145.0	14.5	474	2 B38634	tumor necrosis fac
25	144.0	14.4	277	2 I37552	OX40 homolog - hum
26	142.5	14.2	459	2 I37552	gene murine tumour
27	140.5	14.1	493	2 JC5486	membrane glycoprot
28	138.0	13.8	305	2 A46476	B cell-associated
29	136.5	13.7	1790	1 MMFBI	laminin beta-1 cha

30 130 13.0 256 2 B32393 T-cell antigen 4-1

31 129 12.9 1827 2 T34288 hypothetical prote

32 128.5 12.8 272 2 I48700 gene ox40 protein

33 126.5 12.7 1193 2 A44018 laminin B2t chain

34 125.5 12.6 1192 2 S69000 laminin gamma 2 ch

35 123.5 12.3 255 2 I38426 lymphocyte activat

36 122 12.2 435 2 S40993 hypothetical prote

37 121.5 12.2 1274 2 T42017 cysteine rich prot

38 120 12.0 1609 1 MMHUB2 laminin gamma-1 ch

39 120 12.0 4391 2 A38096 perlecan precursor

40 118 11.8 570 2 T37314 probable kexin (PC

41 118 11.8 942 2 D87803 protein bli-4d (im

42 117 11.7 1548 2 S34583 serine proteinase

43 116 11.6 557 2 A48434 variant-specific s

44 115.5 11.6 1372 2 T25933 hypothetical prote

45 115.5 11.6 1808 2 T15099 hypothetical prote

ALIGNMENTS

RESULT 1

GOMST1

tumor necrosis factor receptor 1 precursor - mouse

N:Alternate names: tumor necrosis factor receptor, 55K

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 01-Dec-2000

C:Accession: A38634; B40254; S16677; S19021; I54532; I57826

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: A38634

A:Molecule type: mRNA

A:Residues: 1-454 <LEW>

A:Cross-references: GB:M60468; NID:g19825; PIDN:AAA39751.1; PID:g19826

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Accession: B40254

A:Molecule type: mRNA

A:Residues: 1-454 <GO2>

A:Cross-references: GB:M60468; NID:g19825; PIDN:AAA39751.1; PID:g19826

R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991

A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro

A:Reference number: S16677; MUID:91285014; PMID:1647956

A:Accession: S16677

A:Molecule type: mRNA

A:Residues: 1-454 <BAR>

A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991

A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A:Reference number: S19021; MUID:92039815; PMID:1657766

A:Accession: S19021

A:Molecule type: mRNA

A:Residues: 1-454 <ROT>

A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R:Bebo, B.F. Immunogenetics 39, 450-451, 1994

A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel

A:Reference number: I54532; MUID:94245292; PMID:8188324

A:Accession: I54532

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-454 <RES>

A:Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733

R:Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M. Mol. Immunol. 30, 165-176, 1993

A:Title: Genomic organization and promoter function of the murine tumor necrosis fact

A:Reference number: I57826; MUID:93156721; PMID:8381516

F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) #status predicted

Query Match 20.5%; Score 205.5; DB 1; Length 455;
Best Local Similarity 31.3%; Pred. No. 1.4e-08;
Matches 53; Conservative 22; Mismatches 75; Indels 17; Gaps

Qy 7 VSSLSHWFLLLLLNLEL-----PVTFAMP-----ESYFNCPDGY----QSNDVCCKTC 53
:
Db 3 LSTVPDLLLVLELVGTPSGVIGLVPHLGDRKRDSVCPQGKYIHPPNNSICCTCK 62
: :

Qy 54 PSGFVEKAPCKIPHTGOCEKCHPGFTGTGDNLGHDELCSLTKCDKNMV--ADCSATSD 111
:
Db 63 HKGYLYNDPCGGQQDTDCRECSGSFFTASENLHRLCLSCSKRKEMGQVEISSCTVD RD 122
: :

Qy 112 RKBCQCIGLY-YDPKPFPESCRCPTKCPOGIPVLQECNSTANTVCS 156
:
Db 123 TVCGCRKNQRYHWSENLFQCFNCSLCNG-TVHLSCQEKKQTIVCT 167
: :

RESULT 4
A6484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A6484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.
J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the
A:Reference number: A6484; MUID:92148151; PMID:1371136
A:Accession: A6484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-327 <BAT>
A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A:Experimental source: BM3 macrophage cell line
A>Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposon
A:Reference number: A47254; MUID:93189576; PMID:7680478
A:Accession: A47254
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Experimental source: MRL lpr/lpr
A>Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853)
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 20.5%; Score 205; DB 2; Length 327;
Best Local Similarity 31.5%; Pred. No. 1.2e-08;
Matches 45; Conservative 23; Mismatches 67; Indels 8; Gaps

Qy 37 NCPDGEYSNDVCCKTSPGSTVFVKAPCKIPTHTGOCEKCHPG-TFTGDKNLGHDELCSLT 95
:
Db 43 NCEGLYOGGFPCQCQPCKKVKDECKMNGTGTPCAPTEKEYMDKNHYADKCRCTL 102
: :

Qy 96 CDKDNQNVAD--CSATSDRKCECQIGLYYYDPKFPESCRCPTKCPQGPVLOECNSTANT 153
:
Db 103 CDBEHGLEVTNCTLTQNTKCKPKD-FYCDSPGCEHCVRCASEBH--TLEPCTATSN 159
: :

Qy 154 VCSSSVSNPRNWFLFLMLIVFCI 176
:
Db 160 NCRK--QSPRNRLWLLTILVLI 180
: :

A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RFT', <X12>
A:Cross-references: DDBJ:D261
A:Experimental source: liver
C:Genetics:

Query Match	19.4%;	Score 194;	DB 2;	Length 324;
Best Local Similarity	27.1%;	Pred. No. 8.2e-08;		
Matches	52;	Conservative 26;	Mismatches 74;	Indels 40;
Gaps				
QY	17	LLLLNLFLPVIFAE-----	-----SYSFNCPGEQSNDVCKCTCP	54
Db	1	MLMTAVLPLVLACPELNVRMQGTDSIFEGLELKRSVRETDNNCSGLYQVGFCCQPCQ	60	
QY	55	SGTEVKAACPXIPHTQGCCKCHPT----	FTGKNDGLHDCLESTCDKQNMVAD--CSA	108
Db	61	PGERKVRDCT--TSGGAPTCPTCEGEYETDRKHYSDKRRCRCAFCDEGHGLEVETNCTR	117	
QY	109	TSDRKCECOIGLXYDPKFFPESCRPCTKCPQGI--PVLOECNSTANTVCCSSYSNPR--NWL	166	
Db	118	TQNTKCRKEN--FCYNASLSDHCYHCTSC--GLEDILEPCTRTSNTKCRKKQSSNYKLLWL	174	
QY	167	FL-----MLIVF	174	
Db	175	LILPGLAIFVF	186	

RESULT 9
JC4302
tumor necrosis factor receptor p55 precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C/Accession: JC4302; PC4093
R/Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A/Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A/Reference number: JC4302; MUID:96011645; PMID:7590278

Query Match 19.4%; Score 193.5; DB 2; Length 461;
Best Local Similarity 32.3%; Pred. No. 1.1e-07;
Matches 41; Conservative 17; Mismatches 58; Indels 11; Gaps 5;
Qy 38 CPDGEY---QSDNVCCCKTSPGSTVFKAPCKIPHTQGOCEKCHPGFTGDKDNLGLHDPCLCS 94

Db	44	CPQSKYSHPNRSCCTCKCHKGTYLHNDCLGPGLDTCRECDNGTFTASENHILTQCLSCS	103
Qy	95	TCDRDQNNV--ADCSATSDRKCCEC--OIGLYYYDPKFPESCRCPTCKPGIPIVLQECNS	149
Db	104	KCRSEMSQVELSPCTVDRDITVCGCRKNQYRKYWSETLF--QCLNCSLCPNG-TVQLPCLE	160
Qy	150	TANTVCS	156
Db	161	KODTICN	167

RESULT 10

apoptosis-mediating surface antigen Fas precursor - human

A:Accession: A40036

N:Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

C:Accession: A40036; S24543; A38142

R:Ittoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, K. Cell 66, 233-243, 1991

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen APO-1. Nucleic Acids Res 19, 113-122, 1991

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <ITO>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krammer, P.H. submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Wu, J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the APO-1 cell surface antigen. Nucleic Acids Res 20, 113-122, 1992

A:Reference number: A38142; MUID:92268122; PMID:1375228

A:Accession: A38142

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134,'Q',136-335 <OE>

A:Experimental source: SKW6.4 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:103810)

A:Note: in NCBI backbone the source is designated as mouse

C:Genetics:

A:Gene: GDB:APT1

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NGA>

F:174-190/Domain: transmembrane #status predicted <TMW>

Query Match	18.9%; Score 189.5; DB 2; Length 335;
Best Local Similarity	30.9%; Pred. No. 1.8e-07;
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Qy	40 DGEYSDVCCCKTCSPTSFVKACKIPHTGOCEKCHPG-TFTGDKNGLHDCELCSTCDK 98 : : : : : : : : : : : : : : : : : : :
Db	50 EGLHHDCQFCHKPCGERKARCTVNGDPPDCVPCEGKEYTDKAHFSSKCRRCRLCDE 109 : : : : : : : : : : : : : : : : : : :
Qy	99 DONMVA--CSATSDRCEQIGLYYYDRFPESCRTKCPGIVPLOECNSTANTVGS 156 : : : : : : : : : : : : : : : : : : :
Db	110 GHGLEVEINCTONTKCRCKPN-FFONSTVFCEHCDPCKECHI--IREKTLSNTKCK 166 : : : : : : : : : : : : : : : : : : :
Qy	157 SSVSNPR-NMLFLML 171
Db	167 EEGRSNLGWLCILL 182

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OM protein - protein search, using sw model

Run on: December 10, 2002, 15:05:57 ; Search time 8.14815 Seconds
(without alignments)
350.834 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MYTFSHVSSLHWFLLLLLL.....SSVSNRNWFLMLLVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues
Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000	100.0	176	10	US-09-855-266A-1
2	858	85.8	148	10	US-09-855-266A-2
3	213.5	21.3	162	10	US-09-798-789-13
4	212.5	21.2	123	10	US-09-855-266A-13
5	209	20.9	461	9	US-09-898-234-15
6	209	20.9	461	9	US-09-899-429A-25
7	209	20.9	461	10	US-09-899-422-15
8	207.5	20.8	162	10	US-09-798-789-15
9	206.5	20.6	355	10	US-09-826-212-14
10	206.5	20.6	355	10	US-09-935-727-16
11	205.5	20.5	201	9	US-09-899-429A-14
12	205.5	20.5	211	9	US-09-899-429A-8
13	205.5	20.5	371	9	US-09-898-234-12
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15	205.5	20.5	455	9	US-09-898-234-2
16	205.5	20.5	455	9	US-09-898-234-17
17	205.5	20.5	455	9	US-09-756-854-5
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19	205.5	20.5	455	9	US-09-899-429A-27

20	205.5	20.5	455	9	US-10-041-574-5	Sequence 5, Appli
21	205.5	20.5	455	10	US-09-826-212-3	Sequence 3, Appli
22	205.5	20.5	455	10	US-09-333-966-5	Sequence 5, Appli
23	205.5	20.5	455	10	US-09-027-287-3	Sequence 3, Appli
24	205.5	20.5	455	10	US-09-874-138-3	Sequence 3, Appli
25	205.5	20.5	455	10	US-09-840-707A-16	Sequence 16, Appli
26	205.5	20.5	455	10	US-09-252-656B-3	Sequence 3, Appli
27	205.5	20.5	455	10	US-09-899-422-2	Sequence 2, Appli
28	205.5	20.5	455	10	US-09-899-422-17	Sequence 17, Appli
29	205.5	20.5	455	10	US-09-935-727-5	Sequence 5, Appli
30	205.5	20.5	455	12	US-10-005-842-3	Sequence 3, Appli
31	205.5	20.5	455	12	US-10-120-397-2	Sequence 2, Appli
32	205	20.5	204	10	US-09-948-018-18	Sequence 18, Appli
33	205	20.5	327	10	US-09-802-669-60	Sequence 66, Appli
34	204.5	20.4	162	10	US-09-798-789-20	Sequence 20, Appli
35	204.5	20.4	285	10	US-09-756-186-6	Sequence 6, Appli
36	203.5	20.3	162	10	US-09-798-789-19	Sequence 19, Appli
37	202.5	20.2	162	10	US-09-798-789-11	Sequence 11, Appli
38	202.5	20.2	349	10	US-09-826-212-13	Sequence 13, Appli
39	202.5	20.2	349	10	US-09-935-727-15	Sequence 15, Appli
40	202	20.2	190	9	US-09-899-429A-18	Sequence 18, Appli
41	202	20.2	200	9	US-09-899-429A-12	Sequence 12, Appli
42	201.5	20.2	162	10	US-09-798-789-14	Sequence 14, Appli
43	201	20.1	371	9	US-09-899-429A-22	Sequence 22, Appli
44	200.5	20.1	153	10	US-09-800-909-3	Sequence 3, Appli
45	200.5	20.1	153	10	US-09-884-987-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

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Gaps	0;						
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Db	1	MYTFSHVSSLHWFLLLLLLFLPVI	FAMPESYSFNC	PDGEGYQSN	DNVCC	KCPG	STFVK 60
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Db	61	APCKIPHTQGQCEKCHPGTFTG	KDNGLDCEL	CTCDKDN	NVADCS	ATSDR	KCECQIGL 120
Qy	121	YYDPKFPESCRCPTKCPQGI	PVLQECN	STANTVC	SSSVSN	PNRNW	FLMLLVFCI 176
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Db   4  YILLLLSCIIIIINSDDITPPEPNSGKCKDNKEYKRHHLLCCLSCPPGTASRLCDSTKNTNT  63
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Db 63 HKGYLYNDPCPGGDTDCRECESGFTASENHLRHLSCSKRCRMGQVEISSCTVDRD 122
QY 112 RKCEQIGLY-YYPDKFPESCRCPTKCPQGPVLAQECNSTANTVCS 156
Db 123 TVCGCRKNQYRHYWSENLFQCFNCSICLNG-TVHLSCQEKQNTVCT 167

RESULT 14
US-09-899-422-12
; Sequence 12, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-899-422-12

Query Match 20.5%; Score 205.5; DB 10; Length 371;
Best Local Similarity 31.3%; Pred. No. 7.4e-10;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNDRVCCKTC 53
Db 3 LSTVPDLLPLVLELLVGIYPSGVLGPHLGDREKRDVSCVPGKYIHPQNNISICCTRC 62
QY 54 PSGTFTVKAPCKIPHTQGOCEKCHPGFTGKDNGLHDCELCSTCDKQNMV--ADCSATSD 111
Db 63 HKGYLYNDPCPGGDTDCRECESGFTASENHLRHLSCSKRCRMGQVEISSCTVDRD 122
QY 112 RKCEQIGLY-YYPDKFPESCRCPTKCPQGPVLAQECNSTANTVCS 156
Db 123 TVCGCRKNQYRHYWSENLFQCFNCSICLNG-TVHLSCQEKQNTVCT 167

RESULT 15
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
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; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-234-2

Query Match 20.5%; Score 205.5; DB 9; Length 455;
Best Local Similarity 31.3%; Pred. No. 8.9e-10;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

QY 7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYFNCPDGEY---QSNDRVCCKTC 53
Db 3 LSTVPDLLPLVLELLVGIYPSGVLGPHLGDREKRDVSCVPGKYIHPQNNISICCTRC 62
QY 54 PSGTFTVKAPCKIPHTQGOCEKCHPGFTGKDNGLHDCELCSTCDKQNMV--ADCSATSD 111
Db 63 HKGYLYNDPCPGGDTDCRECESGFTASENHLRHLSCSKRCRMGQVEISSCTVDRD 122
QY 112 RKCEQIGLY-YYPDKFPESCRCPTKCPQGPVLAQECNSTANTVCS 156
Db 123 TVCGCRKNQYRHYWSENLFQCFNCSICLNG-TVHLSCQEKQNTVCT 167

Search completed: December 10, 2002, 15:08:41
Job time : 9.14815 secs
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